

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 19:17:03 ; Search time 1681.18 Seconds
(without alignments)
15701.003 Million cell updates/sec

Title: US-09-591-500-4
Perfect score: 907
Sequence: 1 gggttcgggtttattgatt.....ctctaatactgccccctgaa 907

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
c 1	836.2	92.2	164945	9	AC089987	AC089987 Homo sapi
2	825.4	91.0	1052	6	AR009985	AR009985 Sequence
3	825.4	91.0	1052	6	I91514	I91514 Sequence 1
4	825.4	91.0	1052	6	I96074	I96074 Sequence 1
5	825.4	91.0	1052	9	HSU73477	U73477 Human acid1
6	822.2	90.7	1136	9	BC007200	BC007200 Homo sapi
7	811.6	89.5	904	9	HSU71084	U71084 Homo sapien
8	796.4	87.8	916	9	HSPHAPI	X75090 H.sapiens m
9	767.4	84.6	925	9	AF025684	AF025684 Homo sapi
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11	716	78.9	70449	9	AC105250	AC105250 Homo sapi
12	702.4	77.4	162482	9	AC022740	AC022740 Homo sapi
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14	700.8	77.3	186886	2	AC016297	AC016297 Homo sapi
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16	623	68.7	1017	10	RATLANP	D32209 Rat mRNA fo
17	607.8	67.0	863	10	AF022957	AF022957 Mus muscu
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19	585	64.5	980	6	AX305936	AX305936 Sequence
20	585	64.5	980	6	I91515	I91515 Sequence 3
21	585	64.5	980	6	I96075	I96075 Sequence 3
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23	571.2	63.0	771	9	BC000608	BC000608 Homo sapi
24	481.8	53.1	1656	9	AY007110	AY007110 Homo sapi
25	484.8	51.2	101819	2	AC129809	AC129809 Rattus no
26	464.8	51.2	170170	2	AC106610	AC106610 Rattus no
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35	330.2	36.4	1475	9	HSU70439	U70439 Human silve
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c 38	313.6	34.6	200445	2	AC105137	AC105137 Homo sapi
c 39	310	34.2	198926	10	AL683843	AL683843 Mouse DNA
40	291.6	32.1	238142	2	AL611930	AL611930 Mus muscu
41	288	31.8	1225	10	AB025581	AB025581 Rattus no
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ALIGNMENTS

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DEFINITION Homo sapiens l2q BAC Rpl1-722Pl1 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
ACCESSION AC089987
VERSION AC089987.26 GI:14277204
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 164945)
AUTHORS Muzny D.M., Adams C., Adio-Oduola B., Ali-Osman F.R., Allen C.,
Alsbrooks S.L., Amaratunge H.C., Are J.R., Banks T., Barbaria J.,

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 QY 61 GAGAGATGGAGATGGCGACAGGATTTCATTTAGAGCTGCGGAACGGGAGCGCCCTCTGATG 120
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 Db 138865 TGAAGAAGCTTTTCTCGGACACAGTCAGTCAATGAAGGCAAACTTGAAGGCGCTTCACAG 138806
 QY 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTACAACTCAAGTAGGCGCTCACTCAATCGCAA 240
 Db 138805 ATGAATTTGAAGAACTGGAAATTCCTTAAGTACAACTCAAGTAGGCGCTCACTCAATTCGAA 138746
 QY 241 ACTTACCAAGTTTAAACAACTTAAAGAACTTGAAGTAACTAGCAAGTAAAGAGCGCTCAGTGG 300
 Db 138745 ACTTGCACAAAGTTAAACAACTTAAAGAACTTGAAGTAACTAGCAAGTAAAGAGCGCTCAGTGG 138686
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 QY 361 AAATTTAAGAACTTCAGCAAAATAGAGCCCGCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 420
 Db 138625 AAATTTAAGAACTTCAGCAAAATAGAGCCCGCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 138566

QY 421 ACCTTTTCACTTCGCGAGGTAAACCAACCTGAACAACCTACTGTGAGAGAAGATGTTTCAAGCTCC 480
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 Db 138505 TCCTGCAACTCACAATATCTCAACGGCTGTGACCCGGATGACAAGAGAGGCCCTTAAGTGG 138446
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 Db 138445 ATGCTGAGGCGCTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 138386
 QY 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGAACCTG 660
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RESULT 2
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 LOCUS AR009985 1052 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 1 from patent US 5756676.
 ACCESSION AR009985
 VERSION AR009985.1 GI:3968790
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 1052)
 AUTHORS Pasternack,G.R.
 TITLE Mammalian protein associated with uncontrolled cell division
 JOURNAL Patent: US 5756676-A 1 26-MAY-1998;
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 BASE COUNT 326 a 196 c 316 g 214 t
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Query Match 91.0%; Score 825.4; DB 6; Length 1052;
 Best Local Similarity 94.4%; Pred. No. 4.2e-162;
 Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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LOCUS I96074 1052 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5734022.
ACCESSION I96074
VERSION I96074.1 GI:3940544
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Antibodies to a novel mammalian protein associated with uncontrolled cell division
JOURNAL Patent: US 5734022-A 1 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..1052
BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN
Query Match 91.0%; Score 825.4; DB 6; Length 1052;
Best Local Similarity 94.4%; Pred. No. 4.2e-162;
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Db 932 CCCTGAA 938
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LOCUS HSU73477 1052 bp mRNA linear PRI 02-JAN-1997
DEFINITION Human acidic nuclear phosphoprotein pp32 mRNA, complete cds.
ACCESSION U73477
VERSION U73477.1 GI:11763272
KEYWORDS .
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Chen,T.-H., Brody,J.R., Romantsev,F.E., Yu,J.-G., Kayler,A.E., Voneiff,E., Kuhajda,F.P. and Pasternack,G.R.
TITLE Structure of pp32, an Acidic Nuclear Protein Which Inhibits Oncogene-Induced Formation of Transformed Foci
JOURNAL Mol. Biol. Cell (1996) In press
REFERENCE 2 (bases 1 to 1052)
AUTHORS Chen,T.-H., Brody,J.R., Romantsev,F.E., Yu,J.-G., Kayler,A.E., Voneiff,E., Kuhajda,F.P. and Pasternack,G.R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-1996) Pathology, The Johns Hopkins University School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA
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BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN
Query Match 91.0%; Score 825.4; DB 9; Length 1052;
Best Local Similarity 94.4%; Pred. No. 4.2e-162;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
Qy 1 GGGTTCGGGGTTATTGATTGAATTCGGCTGGCGGAGCCTCTGCAGAGAGAGCGC 60
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Qy 661 AAGAGGAGGAGTGTGAGTGCAGGAGGAGGAGGAGGATGAAGGTTATACATGAGGAGG 720
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Db	632	ATGATCAAGATGCTCAGGTAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT	691
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BC007200			
LOCUS			
DEFINITION			
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clone MGC:12667 IMAGE:3677623, mRNA, complete cds.			
ACCESSION			
BC007200			
VERSION			
MGC.			
KEYWORDS			
SOURCE			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 1136)			
AUTHORS			
Strausberg, R.			
TITLE			
Direct Submission			
JOURNAL			
Submitted (01-MAY-2001) National Institutes of Health, Mammalian			
Gene Collection (MGC), Cancer Genomics Office, National Cancer			
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
USA			
REMARK			
NIH-MGC Project URL: http://mgc.nci.nih.gov			

COMMENT

Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL plate: 18 Row: j Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5453879.

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BASE COUNT 369 a 207 c 337 g 223 t

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Best Local Similarity 94.2%; Pred. No. 28-161;
Matches 854; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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VERSION	U71084.1	GI:4249365	
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SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Kadkol,S.S., Brody,J.R., Pevsner,J., Bai,J. and Pasternack,G.R.		
JOURNAL	Modulation of oncogenic potential by alternative gene use in human		
REFERENCE	prostate cancer		
AUTHORS	Nat. Med. (1999) In press		
TITLE	Rebel,J.M.J., Kayler,A.E., Kadkol,S.S., Kuhajda,F.P. and		
JOURNAL	Direct Submission		
REFERENCE	Submitted (17-SEP-1996) Pathology, The Johns Hopkins University		
AUTHORS	School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA		
TITLE	Rebel,J.M.J., Kayler,A.E., Kadkol,S.S., Kuhajda,F.P. and		
JOURNAL	Direct Submission		
REFERENCE	Submitted (09-FEB-1999) Pathology, The Johns Hopkins University		
AUTHORS	School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA		
TITLE	Sequence update by submitter		
REMARK	On Feb 9, 1999 this sequence version replaced gi:1916631.		
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Qy	319	AAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAATTAAGAGCTCAGCA	378
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DEFINITION H.sapiens mRNA for HLA-DR associated protein I (PHAPI).
ACCESSION X75090.1 GI:403006
VERSION HLA-DR associated protein I; PHAPI.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Kratzin, H.D.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-1993) H.D. Kratzin, Max Planck Inst. for
Experimental Med., Dept. for Immunochimistry, Hermann-Rein-str. 3,
37075 Goettingen, FRG
REFERENCE 2 (bases 1 to 916)
AUTHORS Vaesen, M., Barnikol-Watanabe, S., Gotz, H., Awl, L.A., Cole, T.,
Zimmermann, B., Kratzin, H.D. and Hilschmann, N.
TITLE Purification and characterization of two putative HLA class II
associated proteins: PHAPI and PHAPII
JOURNAL Biol. Chem. Hoppe-Seyler 375 (2), 113-126 (1994)
MEDLINE 94250340
PUBMED 8192856
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RESULT 9
LOCUS AF025684
DEFINITION Homo sapiens cerebellar leucine rich acidic nuclear protein (LANP)
AF025684
VERSION AF025684.1 GI:2589220
KEYWORDS mRNA, complete cds.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS Matilla, A., Koshy, B.T., Cummings, C.J., Isobe, T., Orr, H.T. and
Zoghbi, H.Y.
TITLE The cerebellar leucine-rich acidic nuclear protein interacts with
ataxin-1
JOURNAL Nature 389 (6654), 974-978 (1997)
MEDLINE 98013170
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PURMED 9353121
REFERENCE 2 (bases 1 to 925)
AUTHORS Matilla,A. and Zoghbi,H.Y.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1997) Molecular and Human Genetics, and Pediatrics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

FEATURES
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BASE COUNT 296 a 169 c 293 g 166 t 1 others

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Query Match 84.6%; Score 767.4; DB 9; Length 925;
Best Local Similarity 94.4%; Pred. No. 5.3e-150;
Matches 795; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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DB 924 CC 925

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DEFINITION complete cds.
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VERSION AF008216.1 GI:2738512
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 5785)
REFERENCE Kadkol,S., Brody,J.R., Pevsner,J., Bai,J. and Pasternack,G.R.
AUTHORS Modulation of oncogenic potential by alternative gene use in human
TITLE prostate cancer
JOURNAL Nature Medicine (1999) In press
REFERENCE 2 (bases 1 to 5785)
AUTHORS Kochevar,G.J., Brody,J.R. and Pasternack,G.R.
TITLE The Structure of a Gene Encoding pp32r1, a New Member of the pp32
Family
JOURNAL Unpublished
AUTHORS 3 (bases 1 to 5785)
TITLE Kochevar,G.J., Brody,J.R. and Pasternack,G.R.
JOURNAL Direct Submission
Submitted (13-JUN-1997) Pathology, Johns Hopkins University School
of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA
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(Mol. Biol. Cell 8(suppl.): 137A, 1997.); similar to other
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GenBank Accession Number U70439, PHAPI2a, encoded by
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[illegible]

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-360H22, 2000 bp overlap;
the clone sequenced to the right is RP11-808H17, 2000 bp overlap.
Actual start of this clone is at base position 97207 of
RP11-360H22; actual end is at base position 22714 of RP11-808H17.

The sequence of AC011026 has been incorporated into AC105250.

FEATURES

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Best Local Similarity 89.2%; Pred. No. 4.3e-139;

Matches 799; Conservative 0; Mismatches 85; Indels 12; Gaps 2;

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Db 124160 ACATATCTTGACGGCTATGACCGGACGACAAAGAGGCCCTCACTTGATGCTGAGGCC 124101
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Db 124100 TACGTGGAGGCCCTGGATGAGGAGGAGGATGAGATGAGGAGGATGATGACGAGAT 124041
QY 612 GCTCAGGTAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 671
Db 124040 GCTCAGGTAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 123993
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Db 123872 GATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 123813
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DEFINITION Homo sapiens chromosome 15, clone RP11-150L8, complete sequence.
ACCESSION AC107992
VERSION AC107992.3 GI:19683511
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 149015)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Ferreira,P., FitzHugh,W., Gage,D., Diaz,J.S., Dodge,S., Faro,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Lakocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Riley,R., Rise,C., Rogov,P.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Unpublished
2 (bases 1 to 149015)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Ferreira,P., FitzHugh,W., Gage,D., Diaz,J.S., Dodge,S., Faro,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Lakocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
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Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149015)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Ferreira,P., FitzHugh,W., Gage,D., Diaz,J.S., Dodge,S., Faro,S.,
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Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 22, 2002 this sequence version replaced gi:18677521.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L24554
Center clone name: 150_L8
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QY 72 ATGGCGACAGGATTCATTTAGAGCTCGGGAACGGAGCGCCTCTGATGTGAAGAAGACTT 131
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Db 86266 GTCCTGGACAACAGTCGGTGCGAATGAAGCAAACTCGAAGGCCCTCACAGATGAATTTCAA 86207
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QY 792 GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 851
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QY	72	ATGGCAGACGGATTCATTTAGAGCTGCGGAACGGAGCCCTCTGATGTGAAGAATTT	131	TITLE	Molecular identification of IIPP2A, a novel potent heat-stable inhibitor protein of protein phosphatase 2A		
Db	66605	ATGGCAGACGGATTCATTTAGAGCTGCGGAACGGAGCCCTCTGATGTGAAGAATTT	66546	JOURNAL	Biochemistry 35 (22), 6998-7002 (1996)		
QY	132	GTCCTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCTCACAGATCAATTTGAA	191	MEDLINE	96240314		
Db	66545	GTCCTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCTCACAGATCAATTTGAA	66486	PUBMED	8679524		
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QY	252	TTAAACAACTTAAGAGCTTGAACCTAAGCAGTAACAGAGCCCTCACTGGCCCTAGAGTA	311	TITLE	Direct Submission		
Db	66425	TTAAACAACTTAAGAGCTTGAACCTAAGCAGTAACAGAGCCCTCACTGGCCCTAGAGTA	66366	JOURNAL	Submitted (13-JUN-1996) Cellular & Molecular Physiology, Pennsylvania State University College of Medicine, 500 University Drive, Hershey, PA 17033, USA		
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DEFINITION	Human potent heat-stable protein phosphatase 2A inhibitor IIPP2A						
ACCESSION	U60823						
VERSION	U60823.1						
KEYWORDS	GI:1408223						
SOURCE	Homo sapiens						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						

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QY 601 GAGGACGTGAGTGAGGAGGAGGAGGATGAGAGGTTATAACGATGGAGAGGTTAGAT 660
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QY 661 GACGAGGAAGATGAGAGAGCTTGGTGAAGAAGAAAGGGTCAGAGCGCAAAACGAGAA 720
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 786 ACTGAAGATGAGGAGAGAGCGATGCCCTAA 815
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 721 CCTGAAGATGAGGAGAGAGATGATGACTAA 750
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: December 8, 2002, 22:43:51
Job time : 1993.18 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 19:14:43 ; Search time 171.199 Seconds
(without alignments)
119.941 Million cell updates/sec

Title: US-09-591-500-4
Perfect score: 907
Sequence: 1 ggggtcggggtttattgatt.....ctctaactctcccctgaa 907

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

-Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	827.8	91.3	906	21	Human prostatic ad
2	825.4	91.0	1052	17	Human pp32 cDNA.
3	825.4	91.0	1052	20	Nucleotide sequenc
4	825.4	91.0	1052	21	Human pp32 nucleot
5	825.4	91.0	1052	24	Human cDNA differe
6	801.6	88.4	1155	23	DNA encoding novel
7	796.4	87.8	916	20	Human V3 loop HIV
8	716	78.9	889	20	Genomic sequence o
9	716	78.9	889	21	Human variant pp32

10	716	78.9	1035	21	AAA88237	Human variant pp32
11	716	78.9	5785	20	AA81535	Genomic sequence o
12	716	78.9	5785	21	AAA88236	Human placenta var
13	681.2	75.1	750	21	AAAI5294	cDNA encoding a pr
14	585	64.5	980	17	AAT27713	Mouse pp32 cDNA cl
15	585	64.5	980	24	ABI99657	Mouse ischaemic co
16	405	44.7	762	13	AAQ21630	pp35-related cDNA
17	405	44.7	762	17	AAT27715	Mouse pp32 cDNA pa
18	330.2	36.4	1371	24	ABK84741	Human cDNA differe
19	328.8	36.3	966	20	AAK60314	DNA encoding a hum
20	257.4	28.4	1588	22	AAK52226	Human polynucleoti
21	249.4	27.5	3453	23	ABV21871	Human prostate exp
22	249.4	27.5	3453	23	ABV22959	Human prostate exp
23	249.4	27.5	3453	23	ABV27701	Human prostate exp
24	249.4	27.5	3453	23	ABV28791	Human prostate exp
c	226	24.9	1863	22	AAH49681	Statmin protein 8
25	213.6	23.6	701	23	AA576388	DNA encoding novel
26	206	22.7	628	24	ABQ59657	Human colon cancer
27	168.4	18.6	1186	15	AAQ57449	U2snRNP A like pro
28	139.2	15.3	1186	23	ABL20435	Drosophila melanog
29	139.2	15.3	1186	23	ABL20435	Drosophila melanog
30	139.2	15.3	1250	23	ABL09961	Xenopus secreted e
31	138.2	15.2	333	21	AAA43216	Human secreted pro
c	129.4	14.3	147	21	AAC20354	Human prostate exp
33	128.4	14.2	450	23	ABV42141	Human colon tumour
34	124.6	13.7	560	24	ABL38556	Human colon tumour
35	109.2	12.0	3489	21	AAA30290	Kaposi's sarcoma-a
36	109.2	12.0	3489	22	AAF82901	Nucleotide sequenc
37	109.2	12.0	3489	24	ABF93487	Kaposi's sarcoma-a
c	109.2	12.0	32207	20	AAV73805	KSHV LTR DNA (nucl
39	109.2	12.0	137507	19	AAV19941	KSHV long unique c
40	106.6	11.8	390	23	AA569541	DNA encoding novel
41	106.2	11.7	303	23	ABL24559	Drosophila melanog
c	106.2	11.7	2403	23	ABL24558	Drosophila melanog
43	106	11.7	575	22	ABA50472	Human breast cell
44	106	11.7	575	22	ABA68422	Human foetal liver
45	106	11.7	575	22	ABA35413	Probe #13879 for g

ALIGNMENTS

RESULT 1

AAA88240

ID AAA88240 standard; DNA; 906 BP.

XX AC AAA88240;

XX DT 15-DEC-2000 (first entry)

XX DE Human prostatic adenocarcinoma consensus pp32 nucleotide sequence.

XX DE Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;

XX KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;

XX KW malignant; cytostatic; gene therapy; ds.

XX OS Homo sapiens.

XX XX WO200045852-A1.

PN 10-AUG-2000.

PD 03-FEB-2000; 2000WO-US02656.

PF 03-FEB-1999; 99US-0118667.

XX PR (UYUJ) UNIV JOHNS HOPKINS.

XX PA Pasternack GR, Bai J;

XX PI WPI; 2000-514896/46.

XX DR Treatment of cancer comprising restoration of pp32 function in

XX PT malignant cells -

Qy 1 GGGTTCGGGTTTATTGATTGATTGATTGCGCTGCGCGCGGAGCCCTCTCCAGAGAGAGAGCCG 60
 Db 32 GGGTTCGGGTTTATTGATTGATTGATTGCGCTGCGCGCGGAGCCCTCTCCAGAGAGAGAGCCG 91
 Qy 61 GAGAGATGGAGATGGGACAGCGGATTCATTAGCTGCGGACCGGAGCCCTCTGATG 120
 Db 92 GAGAGATGGAGATGGGACAGCGGATTCATTAGCTGCGGACCGGAGCCCTCTGATG 151
 Qy 121 TGAAGAACTTTCCTGGACACAGTCGGTCGGAATGAAGCAAACTCGAAGGCCCTCACAG 180
 Db 152 TGAAGAACTTTCCTGGACACAGTCGGTCGGAATGAAGCAAACTCGAAGGCCCTCACAG 211
 Qy 181 ATGAATTTGAAGAACTTTCCTGAGTACATCAATCAACCTGAGCCCTCACTCAATCGCAA 240
 Db 212 ATGAATTTGAAGAACTTTCCTGAGTACATCAATCAACCTGAGCCCTCACTCAATCGCAA 271
 Qy 241 ACTTACCAAAAGTTAAACAACTTTAAGAACTTGAACCTAAGCAGTAAACAGAGCCCTCAGTGG 300
 Db 272 ACTTACCAAAAGTTAAACAACTTTAAGAACTTGAACCTAAGCAGTAAACAGAGCCCTCAGTGG 331
 Qy 301 GCCTAGAACTTTCCTGGACACAGTCGGTCGGAATGAAGCAAACTCGAAGGCCCTCACAG 360
 Db 332 GCCTAGAACTTTCCTGGACACAGTCGGTCGGAATGAAGCAAACTCGAAGGCCCTCACAG 391
 Qy 361 AAATTAAGAACTTTCCTGGACACAGTCGGTCGGAATGAAGCAAACTCGAAGGCCCTCACAG 420
 Db 392 AAATTAAGAACTTTCCTGGACACAGTCGGTCGGAATGAAGCAAACTCGAAGGCCCTCACAG 451
 Qy 421 ACCTTTTCACCTTGGAGGTACCAACCTGAACAACTACTGAGAGAACTTTCCTCAAGCTCC 480
 Db 452 ACCTTTTCACCTTGGAGGTACCAACCTGAACAACTACTGAGAGAACTTTCCTCAAGCTCC 511
 Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGGATGACAGGAGGCCCTCAACTCGG 540
 Db 512 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGGATGACAGGAGGCCCTCAACTCGG 571
 Qy 541 ATGCTGAGGGCTTGTGAGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATG 600
 Db 572 ATGCTGAGGGCTTGTGAGTGCCTGATGATGATGATGATGATGATGATGATGATGATGATG 631
 Qy 601 ATGATGAAGATGCTCAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
 Db 632 ATGATGAAGATGCTCAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 691
 Qy 661 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 Db 692 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 751
 Qy 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 Db 752 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 811
 Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 Db 812 GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 871
 Qy 841 CCTTTTGTGATTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTT 900
 Db 872 CCTATTGTGATTTGACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTT 931
 Qy 901 CCTGAA 907
 Db 932 CCTGAA 938
 RESULT 3
 ID AAX81536
 XX AAX81536 standard; DNA; 1052 BP.
 AC AAX81536;
 XX AAX81536;
 DT 26-AUG-1999 (first entry)
 XX

DE Nucleotide sequence of normal human phosphoprotein 32 (pp32).
 XX Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;
 KW prostatic adenocarcinoma; antineoplastic activity;
 KW transformation suppression; malignant potential; neuroendocrine;
 KW neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.
 XX Homo sapiens.
 OS
 XX W09929906-A2.
 PN
 XX 17-JUN-1999.
 PD
 XX 11-DEC-1998; 98WO-US26433.
 PF
 XX 12-DEC-1997; 97US-0069677.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XI Brody JR, Kadkol SS, Kocheavar GJ, Pasternack GR;
 XX WPI; 1999-385626/32.
 DR
 XX Phosphoprotein 32 (pp32) related genomic sequences
 PT
 XX Example 2; Fig 3; 65pp; English.
 PS
 XX The present sequence represents a human phosphoprotein 32 (pp32)
 CC nucleotide sequence. The specification describes pp32 variants,
 CC associated with cancer in prostate, especially prostatic adenocarcinomas.
 CC Normal pp32 exerts antineoplastic activity through suppression of
 CC transformation. Cancer-associated pp32 variants augment, rather than
 CC inhibit, transformation. Determining the presence of a gene encoding
 CC residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a
 CC diagnostic method for predicting malignant potential of neuroendocrine,
 CC neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.
 XX
 SQ Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;
 Query Match 91.0%; Score 825.4; DB 20; Length 1052;
 Best Local Similarity 94.4%; Pred. No. 2.5e-175;
 Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

CC	modulating GA; M3 is useful for screening an agent capable of modulating	CC
CC	GCA preferably in an inflammation in a tissue; M4 is useful for	CC
CC	detecting an inflammation (especially chronic) in a tissue, an allergic	CC
CC	response in a subject, exposure of a subject to a pathogen or sterile	CC
CC	inflammatory disease (e.g. psoriasis, rheumatoid arthritis,	CC
CC	glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal	CC
CC	reperfusion injury, ARDS, adult respiratory distress syndrome,	CC
CC	inflammatory bowel disease, Crohn's disease, ulcerative colitis,	CC
CC	periodontal disease; also bacterial infection, viral infection,	CC
CC	parasitic infection, protozoal infection, fungal infection and M5 is	CC
CC	useful for treating one of the above conditions. The present	CC
CC	sequence represents a gene differentially expressed in granulocytes.	CC
CC	Note: The sequence data for this patent did not form part	CC
CC	of the printed specification, but was obtained in electronic	CC
CC	format directly from WIPO at	CC
CC	ftp.wipo.int/pub/published_pct_sequences.	CC
xx		xx
sq	Sequence 1052 BP; 326 A; 196 G; 316 G; 214 T; 0 other;	sq
	Query Match 91.0%; Score 825.4; DB 24; Length 1052;	
	Best Local Similarity 94.4%; Pred. No. 2.5e-175;	
	Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;	
Qy	1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGGCTCTGCGAGAGAGAGCGC 60	
Db	32 GGGTTCGGGGTTTATTGATTGAATTCGCCGGCGGGAGGCTCTGCGAGAGAGAGCGC 91	
Qy	61 GAGAGATGGAGTCGGCAGACGGATTCAATTAGAGCTCGGAACGGGACGCCCTCTGATG 120	
Db	92 GAGAGATGGAGTCGGCAGACGGATTCAATTAGAGCTCGGAACGGGACGCCCTCTGATG 151	
Qy	121 TGAAGAAGACTTGTCTCTGCACACACAGTCGGTCCGATGAAGGCAAACTCGAAGGCCCTCACAG 180	
Db	152 TGAAGAAGACTTGTCTCTGCACACACAGTCGGTCCGATGAAGGCAAACTCGAAGGCCCTCACAG 211	
Qy	181 ATGAATTGGAAGACTGGAATCTTAAGTACATCAACGTAGGCCTCACCTCAATCGCAA 240	
Db	212 ATGAATTGGAAGACTGGAATCTTAAGTACATCAACGTAGGCCTCACCTCAATCGCAA 271	
Qy	241 ACTTACCAAAGTTAAACAAACTTAAAGAAGCTTGAAGTAAAGCAAGAGAGAGAGAGAGAGAG 300	
Db	272 ACTTACCAAAGTTAAACAAACTTAAAGAAGCTTGAAGTAAAGCAAGAGAGAGAGAGAGAGAG 331	
Qy	301 GCCTAGAAGTATGCGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360	
Db	332 GCCTAGAAGTATGCGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 391	
Qy	361 AAATTTAAAGACCTCAGCACAATAGAGGCCCTGAAAAGTTAGAAAACCTCGAGAGAGAGAGAG 420	
Db	392 AAATTTAAAGACCTCAGCACAATAGAGGCCCTGAAAAGTTAGAAAACCTCGAGAGAGAGAGAG 451	
Qy	421 ACCTTTTCACCTTGGAGGTAAACCAACCTGAACTACTGTGAGAGAGAGATGTTCAAGCTCC 480	
Db	452 ACCTTTTCACCTTGGAGGTAAACCAACCTGAACTACTGTGAGAGAGAGATGTTCAAGCTCC 511	
Qy	481 TCCTGCAACTCACATATCTCACGGCTGTACCCGATGACAAAGGAGGAGGAGGAGGAGGAGGAG 540	
Db	512 TCCTGCAACTCACATATCTCACGGCTGTACCCGATGACAAAGGAGGAGGAGGAGGAGGAGGAGGAG 571	
Qy	541 ATGTTGAGGGGCTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600	
Db	572 ATGCTGAGGGCTACCTGGAGGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631	
Qy	601 ATGATGAGAGATGCTCAGGTAAATGGAAGATGAGAGGACGAGGATGAGGAGGAGGAGGAGGAG 660	
Db	632 ATGATGGAAGATGCTCAGGTAAATGGAAGATGAGAGGACGAGGATGAGGAGGAGGAGGAGGAGGAG 691	
Qy	661 AAGAGGAGGAGCTGAGTGGAGACGAGGAGGAGGAGGATGAAGGTTATAACAATGGAGAGG 720	
Db	692 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGGTTATAACAATGGAGAGG 751	
Qy	721 TAGATGATGAGGAGATGAAGAAGAGCTTGGTGAAGAGAAAGGGGCTCAGAGCGGAAAT 780	

Db 752 TAGATGACGAGGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAAGAGCGGAAAAAC 811
QY 781 AAGAACTGAAGATGAGGAGAGACGATCCCTAAGTGAATAATCTATTTGAAAAATT 840
Db 812 GAGAACCTGAAGATGAGGAGAGAGATGACTAAGTGAATAACCTATTTGAAAAATT 871
QY 841 CCATTGTGATTTACTGTTTTAGCCGTACCCCTCTCCCCCCCCACACTCTAATCCTGCC 900
Db 872 CCTATTGTGATTTGACTGTTTTTACCACATATCCCTCTCCCCCCCCCTCTAATCCTGCC 931
QY 901 CCTGTAA 907
Db 932 CCTGTAA 938

RESULT 6
AA576389
ID AA576389 standard; cDNA; 1155 BP.
XX
AC AA576389;
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #12193.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG12202.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 12193; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA564197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1155 BP; 340 A; 219 C; 347 G; 249 T; 0 other;

Query Match 88.4%; Score 801.6; DB 23; Length 1155;
Best Local Similarity 93.4%; Pred. No. 5.4e-170;
Matches 848; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 1 GGGTTCGGGGTTTATGATTGAATTCGGCTGGCGCGGAGGCTCTGAGAGAGAGAGCGC 60
Db 57 GGGTTCGGGGTTTATGATTGAATTCGGCGCGGCGGAGGCTCTGAGAGAGAGAGCGC 116
QY 61 GAGAGATGGAGATGGCAGACGGATTCTATTTAGAGCTGCGGAACGGACGCCCTCTCATG 120
Db 117 GAGAGATGGAGATGGCAGACGGATTCTATTTAGAGCTGCGGAACAGGACGCCCTCTCATG 176
QY 121 TGAAGAAGACTTGTCTTGAGACCAACAGTCGGTGAATGAAGGCAAACTCGAAGGCTCTACAG 180
Db 177 TGAAGAAGACTTGTCTTGAGACCAACAGTCGGTGAATGAAGGCAAACTCGAAGGCTCTACAG 236
QY 181 ATGAATTTGAAGAAGCTGAAATTTTAAAGTACAATCAACGTAGGCTCACCTCAATCGCAA 240
Db 237 ATGAATTTGAAGAAGCTGAAATTTTAAAGTACAATCAACGTAGGCTCACCTCAATCGCAA 296
QY 241 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG 300
Db 297 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTAAGCAGTAACAGAGTCTCAGGG 356
QY 301 CCCTAGAGATTTGGCAGAAAAGTGTCCAAACCTCTATCATCTAATTTAAGTGGCAAC 359
Db 357 CCCTAGAGATTTGGCAGAAAAGTGTCCAAACCTCTATCATCTAATTTAAGTGGCAAC 416
QY 360 AAAATTTAAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACTTCGAGAGCTTA 419
Db 417 AAAATTTAAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACTTCGAGAGCTTA 476
QY 420 GACCTTTTTCACCTTCGAGAGTAACCAACCTGAACAACTACTGAGAGAGAGATGTTCACAGCTC 479
Db 477 GACCTTTTTCACCTTCGAGAGTAACCAACCTGAACAACTACTGAGAGAGAGATGTTCACAGCTC 536
QY 480 CTCCTGCAACTCACAATATCTCAACGGCTGTGCCCGGATGACAAGGAGGCCCTCACTACG 539
Db 537 CTCCTGCAACTCACAATATCTCAACGGCTGTGCCCGGATGACAAGGAGGCCCTCACTACG 596
QY 540 GATGCTGAGGGCTTTGTGGAGTGCCTGATGACAAGGAGGAGGATGAGGATGAGGAGGAG 599
Db 597 GATGCTGAGGGCTACGTTGAGGGCTGTGATGAGGAGGAGGATGAGGATGAGGAGGAG 656
QY 600 TATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAG 659
Db 657 TATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAG 716
QY 660 GAAGAGAGGAGGATGAGTGGAGAGGAGGAGGAGGAGGATGAGGATGAGGAGGAGGAG 719
Db 717 GAAGAGAGGAGGATGAGTGGAGAGGAGGAGGAGGAGGATGAGGATGAGGAGGAGGAG 776
QY 720 GTAGATGATGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 779
Db 777 GTAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 836
QY 780 TAGAAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 839
Db 837 CGAAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 896
QY 840 TCCTTTTGTGATTTTACTGTTTTTACCGGTACCCCTCTCCCCCCCCACTCTAATCCTGC 899
Db 897 TCCTTTTGTGATTTTACTGTTTTTACCGGTACCCCTCTCCCCCCCCACTCTAATCCTGC 956
QY 900 CCCTGTAA 907
Db 957 CCCTGTAA 964

RESULT 7	
AAV1743	
ID	AAV1743 standard; cDNA; 916 BP.
XX	
AC	AAV1743;
XX	
DT	15-MAR-1999 (first entry)
XX	
DE	Human V3 loop HIV receptor p30/PHAPI cDNA.
XX	
KW	HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;
KW	P30 protein; PHAPI; infection; therapy; diagnosis; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	CDS
FT	104...853
FT	/*tag- a
XX	
PN	W09840480-A1.
XX	
PD	17-SEP-1998.
XX	
PF	12-MAR-1998; 98WO-EP01409.
XX	
PR	12-MAR-1997; 97US-0040969.
XX	
PA	(CNRS) CENT NAT RECH SCI.
PA	(INSP) INST PASTEUR.
XX	
PI	Briand J, Callebaut C, Guichard G, Hovanessian A;
PI	Jacotot E, Krust B, Muller S;
XX	
DR	WPI; 1999-034588/03.
DR	P-PSDB; AAW84053.
XX	
PT	New isolated V3 loop HIV receptor - comprises P95/nucleolin,
PT	P40/PHAPI and P30/PHAPI proteins, used to develop products for the
PT	treatment and prevention of HIV infection
XX	
PS	Claim 17; Fig 49(12); 267pp; English.
CC	This cDNA sequence codes for the P30 (or PHAPI) protein of the
CC	newly identified V3 loop HIV receptor. This novel protein complex
CC	receptor for HIV retroviruses consists of an association of 3
CC	proteins named P95/nucleolin, P40/PHAPI and P30/PHAPI (see
CC	AAW84052-54). These proteins were isolated from human CD4+ CEM
CC	T-cell extracts using an affinity matrix containing either the
CC	pseudopeptide 5(KpsIcH2)NPR)-template assembled synthetic peptide
CC	or a synthetic V3 loop peptide (see AAW84055). P30 was identified
CC	as PHAPI by amino acid sequence analysis. The invention also
CC	concerns peptidic or non-peptidic molecules having the ability to
CC	alter and/or prevent the binding of the novel HIV receptor to the
CC	HIV retrovirus, and to pharmaceutical and diagnostic compositions
CC	containing such molecules. Methods are provided for screening for
CC	new active molecules, and to methods of screening genetic defects
CC	in the expression of the V3 loop HIV receptor in individuals that
CC	survive long-term HIV infection or who are HIV-resistant. Such
CC	genetically defective polynucleotides can be used in gene therapy.
XX	
SQ	Sequence 916 BP; 296 A; 167 C; 275 G; 178 T; 0 other;
Query Match	87.8%; Score 796.4; DB 20; Length 916;
Best Local Similarity	94.2%; Pred. No. 7.4e-169;
Matches 827; Conservative	0; Mismatches 51; Indels 0; Gaps 0;
QY	1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGGAGCCTCTGCAGAGAGAGAGCGC 60
DB	39 GGGTTCGGGGTTTATTGATTGAATTCGCCCGCGGGAGCCTCTGCAGAGAGAGAGCGC 98
QY	61 GAGAGATGGAGATGGCGAGACGGATTTCATTTAGAGCTCGCGAAGCGGACGCCCTCTGATG 120
DB	99 GAGAGATGGAGATGGCGAGACGGATTTCATTTAGAGCTCGCGAAGCGGACGCCCTCTGATG 158

QY	121	TGAAGAACCTTGTCTCTGGACAACAGTCGGTCGAATGAAGCAAACTCGAAGGCCTCACAG	180
DB	159	TGAAGAACCTTGTCTCTGGACAACAGTCGGTCGAATGAAGCAAACTCGAAGGCCTCACAG	218
QY	181	ATGAATTTGAAGAAGTGAATTTCTTAAGTACAATCAAGTAGGCGCTCACCTCAATCGCAA	240
DB	219	ATGAATTTGAAGAAGTGAATTTCTTAAGTACAATCAAGTAGGCGCTCACCTCAATCGCAA	278
QY	241	ACTTACCAGGTTAAACAACTTAAGAAGCTTGAACCTTAAGCAAGTAACAGAGCCCTCAGTGG	300
DB	279	ACTTACCAGGTTAAACAACTTAAGAAGCTTGAACCTTAAGCAAGTAACAGAGCTCTCAGGGG	338
QY	301	GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	360
DB	339	GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	398
QY	361	AAATTTAAAGAGCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAACCTCAGAGAGCTTAG	420
DB	399	AAATTTAAAGAGCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAACCTCAGAGAGCTTAG	458
QY	421	ACCTTTTCACTTGCAGAGTAAACCAACCTGACAACTACTGACAGAGAGATGTTCAAGCTCC	480
DB	459	ACCTTTTCACTTGCAGAGTAAACCAACCTGACAACTACTGACAGAGAGATGTTCAAGCTCC	518
QY	481	TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTAACTCGG	540
DB	519	TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTAACTCGG	578
QY	541	ATGGTGAGGGCTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGT	600
DB	579	ATGGTGAGGGCTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGT	638
QY	601	ATGATGAAGATGCTCAGGTAATGCGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT	660
DB	639	ATGATGAAGATGCTCAGGTAATGCGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT	698
QY	661	AAGAGGAGGAGCTGAGTGGAGACGAGGAGGAGGAGGATGAAGCTTATACAAATGGAGAGG	720
DB	699	AAGAGGAGGAGCTGAGTGGAGACGAGGAGGAGGAGGATGAAGCTTATACAAATGGAGAGG	758
QY	721	TAGATGATGAGGAAGATGAAGAAGCTTGTGTAAGAAGAAAGGGGTGAGAGCGCAAAAT	780
DB	759	TAGATGATGAGGAAGATGAAGAAGCTTGTGTAAGAAGAAAGGGGTGAGAGCGCAAAAT	818
QY	781	AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840
DB	819	GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	878
QY	841	CCCTTTGTGATTTTACTGTTTTTGTAGCCGTACCCCTCT	878
DB	879	CCCTTTGTGATTTGACTGTTTTTACCCTATCCCTCT	916
RESULT 8			
AAW81537			
ID	AAW81537 standard; DNA; 889 BP.		
XX			
AC	AAW81537;		
XX			
DT	26-AUG-1999 (first entry)		
XX			
DE	Genomic sequence of phosphoprotein 32 variant pp32r2.		
XX			
KW	Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;		
KW	prostatic adenocarcinoma; antineoplastic activity;		
KW	transformation suppression; malignant potential; neuroendocrine;		
KW	neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0929906-A2.		
XX			

PD 17-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US26433.
XX
PR 12-DEC-1997; 97US-0069677.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Brody JR, Kadkol SS, Kocheavar GJ, Pasternack GR;
XX WPI; 1999-385626/32.
DR
XX
PT Phosphoprotein 32 (pp32) related genomic sequences
PS Claim 1; Fig 5; 65pp; English.
XX
CC The present sequence represents the genomic sequence of phosphoprotein
CC 32 (pp32) variant pp32r2. The pp32r1 and pp32r2 sequences are associated
CC with cancer in prostate, especially prostatic adenocarcinomas. Normal
CC pp32 exerts antineoplastic activity through suppression of
CC transformation. Cancer-associated pp32 variants augment, rather than
CC inhibit, transformation. Determining the presence of a gene encoding
CC residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a
CC diagnostic method for predicting malignant potential of neuroendocrine,
CC neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.
XX
SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 78.9%; Score 716; DB 20; Length 889;
Best Local Similarity 89.2%; Pred. No. 7.4e-151;
Matches 799; Conservative 0; Mismatches 85; Indels 12; Gaps 2;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGAGGAGGCTCTGCAGAGAGAGCGC 60
DB 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGAGGAGGCTCTGCAGAGAGAGCGC 60

QY 61 GAGAGATGAGATGGGACGCGATTCATTAGACTCGGGAACGGGAGCGGCTCTGATG 120
DB 61 GAGAGATGAGATGGGACGCGATTCATTAGACTCGGGAACGGGAGCGGCTCTGATG 120

QY 121 TGAAGAAGTCTTCTGGACACAGTCGCTGAATGAAGGCAAACTCGAAGCGCTCAG 180
DB 121 TGAAGAAGTCTTCTGGACACAGTCGCTGAATGAAGGCAAACTCGAAGCGCTCAG 180

QY 181 ATGAATTTGAAGAACTGGAATTTAAGTACAACTAGGCTACCTCAATTCGCA 240
DB 181 ATGAATTTGAAGAACTGGAATTTAAGTACAACTAGGCTACCTCAATTCGCA 240

QY 241 ACTTACCAAGTTAAACAACTTAAGAAGCTTGAACCTAGCAGTAACAGAGCCCTCAGTGG 300
DB 241 ACTTACCAAGTTAAACAACTTGAAGCTTGAACCTAGCAGTAACAGAGCCCTCAGTGG 300

QY 301 GCCTAGAAGTATTGGCAGAAAGTGTCCAACTCATACATCTAAATTTAAGTGGCAACA 360
DB 301 GCCTAGAAGTATTGGCAGAAAGTGTCCAACTCATACATCTAAATTTAAGTGGCAACA 360

QY 361 AAATTAAGACCTCAGCACATAGAGCCCTGAAAGATTGAAAACCTCGAGAGCTTAG 420
DB 361 AAATTAAGACCTCAGCACATAGAGCCCTGAAAGATTGAAAACCTCGAGAGCTTAG 420

QY 421 ACCTTTTCACTTGGGAGTAAACCACTGAACCTTACTGAGGAGAGATGTTCAAGCTCC 480
DB 421 ACCTTTTCACTTGGGAGTAAACCACTGAACCTTACTGAGGAGAGATGTTCAAGCTCC 480

QY 481 TCCTGCAACTCACAATCTCAACGGCTGTGACCCGGATGACAGAGGCGCCCTAACTCGG 540
DB 481 TCCTGCAACTCACAATCTCAACGGCTGTGACCCGGATGACAGAGGCGCCCTAACTCGG 540

QY 541 ATGTTGAGGGCTTTGTGGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600
DB 541 ATGTTGAGGGCTTTGTGGAGTGGCTGATGACAGAGGAGGAGGATGAGGATGAGGAGGAGT 600

QY 601 ATGATGAAGATGCTCAGGTAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
DB 601 ATGATGAAGATGCTCAGGTAATGAAGATGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660

DB 589 ATGATGAAGATGCTCAGGTAATGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 648
QY 661 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB 649 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708
QY 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 709 TAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 768
QY 781 AAGAACTGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 769 GAGAACTGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 828
QY 841 CCTTTTGTGATTTTACTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 896
DB 829 CCTATTGTGATTTGACTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 884

RESULT 9
AAA88239
ID AAA88239 standard; DNA; 889 BP.
XX
AC AAA88239;
XX
DT 15-DEC-2000 (first entry)
XX
DE Human variant pp32r2 genomic DNA sequence.
XX
KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200045852-A1.
XX
PD 10-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US02656.
XX
PR 03-FEB-1999; 99US-0118667.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Pasternack GR, Bai J;
XX
DR WPI; 2000-514896/46.
XX
PT Treatment of cancer comprising restoration of pp32 function in
PT malignant cells -
XX
PS Example 5; Fig 5; 90pp; English.
XX
CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human variant pp32r2 genomic DNA sequence from
CC an example of the present invention.
XX
SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 78.9%; Score 716; DB 21; Length 889;
Best Local Similarity 89.2%; Pred. No. 7.4e-151;

Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL; acidic protein rich in leucine; chromosome 15q25; tumour suppressor; K12; K13; K14; K15; K16; K17; K18; K19; K20; K21; K22; K23; K24; K25; K26; K27; K28; K29; K30; K31; K32; K33; K34; K35; K36; K37; K38; K39; K40; K41; K42; K43; K44; K45; K46; K47; K48; K49; K50; K51; K52; K53; K54; K55; K56; K57; K58; K59; K60; K61; K62; K63; K64; K65; K66; K67; K68; K69; K70; K71; K72; K73; K74; K75; K76; K77; K78; K79; K80; K81; K82; K83; K84; K85; K86; K87; K88; K89; K90; K91; K92; K93; K94; K95; K96; K97; K98; K99; K100; K101; K102; K103; K104; K105; K106; K107; K108; K109; K110; K111; K112; K113; K114; K115; K116; K117; K118; K119; K120; K121; K122; K123; K124; K125; K126; K127; K128; K129; K130; K131; K132; K133; K134; K135; K136; K137; K138; K139; K140; K141; K142; K143; K144; K145; K146; K147; K148; K149; K150; K151; K152; K153; K154; K155; K156; K157; K158; K159; K160; K161; K162; K163; K164; K165; K166; K167; K168; K169; K170; K171; K172; K173; K174; K175; K176; K177; K178; K179; K180; K181; K182; K183; K184; K185; K186; K187; K188; K189; K190; K191; K192; K193; K194; K195; K196; K197; K198; K199; K200; K201; K202; K203; K204; K205; K206; K207; K208; K209; K210; K211; K212; K213; K214; K215; K216; K217; K218; K219; K220; K221; K222; K223; K224; K225; K226; K227; K228; K229; K230; K231; K232; K233; K234; K235; K236; K237; K238; K239; K240; K241; K242; K243; K244; K245; K246; K247; K248; K249; K250; K251; K252; K253; K254; K255; K256; K257; K258; K259; K260; K261; K262; K263; K264; K265; K266; K267; K268; K269; K270; K271; K272; K273; K274; K275; K276; K277; K278; K279; K280; K281; K282; K283; K284; K285; K286; K287; K288; K289; K290; K291; K292; K293; K294; K295; K296; K297; K298; K299; K300; K301; K302; K303; K304; K305; K306; K307; K308; K309; K310; K311; K312; K313; K314; K315; K316; K317; K318; K319; K320; K321; K322; K323; K324; K325; K326; K327; K328; K329; K330; K331; K332; K333; K334; K335; K336; K337; K338; K339; K340; K341; K342; K343; K344; K345; K346; K347; K348; K349; K350; K351; K352; K353; K354; K355; K356; K357; K358; K359; K360; K361; K362; K363; K364; K365; K366; K367; K368; K369; K370; K371; K372; K373; K374; K375; K376; K377; K378; K379; K380; K381; K382; K383; K384; K385; K386; K387; K388; K389; K390; K391; K392; K393; K394; K395; K396; K397; K398; K399; K400; K401; K402; K403; K404; K405; K406; K407; K408; K409; K410; K411; K412; K413; K414; K415; K416; K417; K418; K419; K420; K421; K422; K423; K424; K425; K426; K427; K428; K429; K430; K431; K432; K433; K434; K435; K436; K437; K438; K439; K440; K441; K442; K443; K444; K445; K446; K447; K448; K449; K450; K451; K452; K453; K454; K455; K456; K457; K458; K459; K460; K461; K462; K463; K464; K465; K466; K467; K468; K469; K470; K471; K472; K473; K474; K475; K476; K477; K478; K479; K480; K481; K482; K483; K484; K485; K486; K487; K488; K489; K490; K491; K492; K493; K494; K495; K496; K497; K498; K499; K500; K501; K502; K503; K504; K505; K506; K507; K508; K509; K510; K511; K512; K513; K514; K515; K516; K517; K518; K519; K520; K521; K522; K523; K524; K525; K526; K527; K528; K529; K530; K531; K532; K533; K534; K535; K536; K537; K538; K539; K540; K541; K542; K543; K544; K545; K546; K547; K548; K549; K550; K551; K552; K553; K554; K555; K556; K557; K558; K559; K560; K561; K562; K563; K564; K565; K566; K567; K568; K569; K570; K571; K572; K573; K574; K575; K576; K577; K578; K579; K580; K581; K582; K583; K584; K585; K586; K587; K588; K589; K590; K591; K592; K593; K594; K595; K596; K597; K598; K599; K600; K601; K602; K603; K604; K605; K606; K607; K608; K609; K610; K611; K612; K613; K614; K615; K616; K617; K618; K619; K620; K621; K622; K623; K624; K625; K626; K627; K628; K629; K630; K631; K632; K633; K634; K635; K636; K637; K638; K639; K640; K641; K642; K643; K644; K645; K646; K647; K648; K649; K650; K651; K652; K653; K654; K655; K656; K657; K658; K659; K660; K661; K662; K663; K664; K665; K666; K667; K668; K669; K670; K671; K672; K673; K674; K675; K676; K677; K678; K679; K680; K681; K682; K683; K684; K685; K686; K687; K688; K689; K690; K691; K692; K693; K694; K695; K696; K697; K698; K699; K700; K701; K702; K703; K704; K705; K706; K707; K708; K709; K710; K711; K712; K713; K714; K715; K716; K717; K718; K719; K720; K721; K722; K723; K724; K725; K726; K727; K728; K729; K730; K731; K732; K733; K734; K735; K736; K737; K738; K739; K740; K741; K742; K743; K744; K745; K746; K747; K748; K749; K750; K751; K752; K753; K754; K755; K756; K757; K758; K759; K760; K761; K762; K763; K764; K765; K766; K767; K768; K769; K770; K771; K772; K773; K774; K775; K776; K777; K778; K779; K780; K781; K782; K783; K784; K785; K786; K787; K788; K789; K790; K791; K792; K793; K794; K795; K796; K797; K798; K799; K800; K801; K802; K803; K804; K805; K806; K807; K808; K809; K810; K811; K812; K813; K814; K815; K816; K817; K818; K819; K820; K821; K822; K823; K824; K825; K826; K827; K828; K829; K830; K831; K832; K833; K834; K835; K836

Db	4628	AC	TTACCAAGTTA---AAGTTGAGAAAGCTTGAAC	TAACTA-----AGAGTCTCAGGGG	4675				
Qy	301	GC	CTAGAAGTATTGGCAGAAAAAGTCTCCAAACCTCATACAT	CTAAATTTTAAGTGGCAACA	360				
Db	4676	GC	CTGGAGTATTGGCAGAAAAAGTCTCCAAACCTCACGCAT	CTATATTTAAGTGGCAACA	4735				
Qy	361	AA	ATTAAAGACCTTCAGCACAATAGAGCCCTCGAAAGGTT	TAGAAAACCTCGAGAGCTTAG	420				
Db	4736	AA	ATTAAAGACCTTCAGCACAATAGAGCCCTCGAAAGGTT	TAGAAAACCTCAAGAGCTTAG	4795				
Qy	421	AC	CTTTTTCACCTTCGAGGTTAAACCAACCTGAACAACT	ACTCTGAGAGAGATGTTCAAGCTCC	480				
Db	4796	AC	CTTTTTCAAATTCGAGGTTAAACCAACCTGAACAACT	ACTCGGAGAGAAACGTGTTCAAGCTTC	4855				
Qy	481	TC	CTGCAACCTTCACATATCTCAACGGCTGTGACCCGGAT	GCACAAGGAGGCCCTTAACCTCGG	540				
Db	4856	TC	CTGCAACCTTCACATATCTGACAGCTGTTACTGGGACC	ACACAGGAGGCCCTTACTCAG	4915				
Qy	541	AT	GTGTAGGCGTTTGTGGAGTGCCTGGATGACACAGGAG	GAGATGAGGATGAGGAGGAGT	600				
Db	4916	AT	TTGAGGACCAGCTGGAGGGCTTGGATGACGAGGAGG	GGGTGAGCATGAGGAGGAGT	4975				
Qy	601	AT	GATGAGATGCTCAGGTAAATGGAAGATGAGGAGGAG	CAGGATCAGGAGGAGGAACGTG	660				
Db	4976	AT	GATGAGATGCTCAGGTAGTGGAAAGATGAGGAGGGC	CGAGGAGGAGGAGGAGGAGT	5035				
Qy	661	AA	GAGGAGGACGTGAGTGGAGACGAGGAGGAGCAAGGAT	CAAGGTTATAACAATGGAGAGG	720				
Db	5036	AA	GAGGAGGACGTGAGTGGAGGAGGACGAGGAGATGA	AGAGGTTATAAACGATGGAGAGG	5095				
Qy	721	TAG	ATGATGATGAGGAAAGATGAAGAAGAGCTTGGTGA	AGAAAGGGGTGAGAGCGCAAAAT	780				
Db	5096	TAG	ATGATGATGAGGAAAGATGAAGAAGAGCTTGGTGA	AGAAAGGGGTGAGAGCGCAAAAT	5155				
Qy	781	AA	GAACCTGAAGATGAGGAGAGAGCATGCCTAAGTGA	ATAATCTATTTTGAATAATT	840				
Db	5156	GAGA	ACCTGAAGATGAGGAGAGAGATGATGACTAAGTA	AGAATAACCTATTTTGAATAATT	5215				
Qy	841	CT	TTTCTGATTTTACTGTTTTTTAGCCGTACCCCTCTC	CCCCCCCCACTCTAATCC	896				
Db	5216	CT	ATTGATGATTTGACATGTTTTTACCATATCCCTCC	CCCCCTCCCAATCCCTGCCCC	5271				
RESULT 13									
AAAL5294									
ID	AAAL5294 standard; cDNA; 750 BP.								
XX	AAAL5294;								
XX									
DT	04-SEP-2000 (first entry)								
DE	cDNA encoding a protein phosphatase 2A inhibitor.								
XX	Syndecan-4; angiogenesis; proteoglycan; protein kinase C;								
KW	delta-isoenzyme; alpha isoenzyme; protein phosphatase; infarction;								
KW	endothelial cell proliferation; endothelial cell migration; anoxia;								
XX	myocardial infarction; chronic myocardial ischemia; heart tissue; ss.								
OS	Homo sapiens.								
XX									
FH	Key	Location/Qualifiers							
FT	CDS	1..750							
FT		/*tag= a							
XX									
PN	W0200027416-A1.								
XX									
PD	18-MAY-2000.								
XX									
PF	10-NOV-1999; 99WO-US26647.								
XX									
PR	12-NOV-1998; 98US-0190976.								
XX									

PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX	
PI	Simons M, Horowitz A;
XX	
DR	WPI: 2000-376307/32..
DR	P-PSDB; AAY93262.
XX	
PT	Stimulating angiogenesis, useful particularly for treating cardiac
PT	anoxia and infarction, by preventing phosphorylation of specific
PT	residue in syndecan-4, present in endothelial cells -
XX	
PS	Disclosure; Page 35; 73pp; English.
XX	
CC	The present sequence encodes a protein phosphatase 2A inhibitor. The
CC	protein phosphatase 1 is used in the method of the invention. The
CC	specification describes a method for stimulating angiogenesis within
CC	variable cells, tissues, or organs in situ. The method comprises
CC	treating target endothelial cells such that Ser183, in the
CC	intracellular cytoplasmic domain of syndecan-4 proteoglycan, is
CC	present in non-phosphorylated form in at least some syndecan-4 molecules.
CC	The cells are treated with an inhibitor of syndecan-4 protein kinase C
CC	(PKC) delta-isoenzyme, an agent that increases intracellular activity of
CC	the PKC alpha-isoenzyme, or an agent that activates at least one of
CC	protein phosphatases 1 or 2A. Keeping Ser183 in the non-phosphorylated
CC	form results in activation of protein kinase C alpha isoenzyme, which is
CC	essential for endothelial cell proliferation and migration in situ.
CC	Syndecan-4 participates in intracellular signalling through
CC	oligomerisation of its cytoplasmic tail and this process does not
CC	occur if Ser183 is phosphorylated. The method can be used in vivo or
CC	in vitro, to stimulate angiogenesis in cells or tissues which are
CC	defective or have suffered anoxia or infarction, particularly myocardial
CC	infarction, or chronic myocardial ischemia of heart tissue, and to
CC	study mechanisms involved in control of angiogenesis.
XX	
SO	Sequence 750 BP; 260 A; 130 C; 229 G; 131 T; 0 other;
<p>Query Match 75.1%; Score 681.2; DB 21; Length 750; Best Local Similarity 94.3%; Pred. No. 4.3e-143; Matches 707; Conservative 0; Mismatches 43; Indels 0; Gaps 0</p>	
Qy	66 ATGAGATGGCAGACGGATTCTATTAGAGCTGCGGAACGGAGCCCTCTGATGTGAAA 125
Db	1 ATGAGATGGCAGACGGATTCTATTAGAGCTGCGGAACGGAGCCCTCTGATGTGAAA 60
Qy	126 GAACCTTGCTCGACACACAGTCGGTTCGAATGAAGGCAACCTCGAAGGCCTCACAGATGAA 185
Db	61 GAACCTTGCTCGACACACAGTCGGTTCGAATGAAGGCAACCTCGAAGGCCTCACAGATGAA 120
Qy	186 TTTGAGAAGCTGGAATCTTAAGTCAATCAAGTAGCCCTCACTCAATGCGAAACCTTA 245
Db	121 TTTGAGAAGCTGGAATCTTAAGTCAATCAAGTAGCCCTCACTCAATGCGAAACCTTA 180
Qy	246 CCAAAGTTAAACAAACTTAAGAGCTTGACTTAAGCAGTACACAGGCTCAGTGGGCGCTA 305
Db	181 CCAAAGTTAAACAAACTTAAGAGCTTGACTTAAGCAGTACACAGGCTCAGTGGGCGCTG 240
Qy	306 GAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAATTT 365
Db	241 GAAGTATTGGCAGAAAAGTGTCCGAACCTCAGCATCTAAATTTAAGTGGCAACAAATTT 300
Qy	366 AAGAGCCTCAGCACAAATAGAGCCCTCGAAAAGTTAGAAAACCTCAAGAGCTTAGACCTT 425
Db	301 AAGAGCCTCAGCACAAATAGAGCCCTCGAAAAGTTAGAAAACCTCAAGAGCTTAGACCTT 360
Qy	426 TTCACCTTGGAGGTAAACCACTGAAACAACCTACTCTAGAGAGAAGATGTTCAAGCTCTCCTG 485
Db	361 TTCACCTTGGAGGTAAACCACTGAAACAACCTACTCTAGAGAGAAGATGTTCAAGCTCTCCTG 420
Qy	486 CAACTCACATATCTCAACGGCTGTCAACCGGATGACAGAGGAGGCCCTCACTCGGATGGT 545
Db	421 CAACTCACATATCTCGACGGCTATGACCCGGAGACAGAGGAGGCCCTCACTCGGATGGT 480
Qy	546 GAGGGCTTTGTGGAGTGCCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGTATGAT 605

Db	10	AGAGAGCGCGAGAGATGGAGTGGACAAACGGATTTATTTAGAGCTGCGGACAGGAC	69
Qy	110	GCCTCTCATGTGAAGAACATTGCTTGGACACACAGTCGGTCGNATCAAGGCAAACTCGA	169
Db	70	GCCTCTCATGTGAAGAGCTGGCTCGGTAACCTGTAAGTCAATTGAAGGCAAAATTCGA	129
Qy	170	AGGCTTCACAGATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACCTAGGCTTCAC	229
Db	130	AGGCTTCACGGATGAGTTTGAGAACTGGAAATTCCTTAAGTACAATCAACCTAGGCTTCAC	189
Qy	230	CTCAATCGCAAACTTTACCAAAAGTTAAACAACCTTAAGAAGCTTGAACCTTAAGCAGTAACAG	289
Db	190	CTCCATTTCCAACTTTACCAAAAGTTAAACAACCTCAAGAAGCTTGAATTAAGCGAAAAACAG	249
Qy	290	AGCCTCAGTGGGCCCTAGAGATATTGGCGAAGAAAGTGTCCAAACCTCATACATCTAAATTT	349
Db	250	AATCTCAGGGGACCTGGAGTATTGGCAGAGAAATGTCCGAACCTTAAGCATCTAAATTT	309
Qy	350	AAGTGGCAACAAATTAAGACCTCAGACACAATAGAGCCCTGAAAAAGTTAGAAAACT	409
Db	310	AAGTGGCAACAAATTAAGAGATCTCAGCACAAATAGAGCCGTGAAGAAGTTAGAAATCT	369
Qy	410	CGAGAGCTTTAGACCTTTTCACTTGGCAGGTAAACCAACCTGAACAACTACTGAGAGAAGAT	469
Db	370	CAGAAGCTTAGACCTTTTAACTGTGAGGTGACCAACCTGAATGCTTACCGAGAAAAAGT	429
Qy	470	GTTCAAGCTCCTCTCGCAACTCACATATCTCAACGGCTGTGACCCGGATGACNAGGAGGC	529
Db	430	GTTCAAGCTCCTGCCCCAGGTCATGTACCTCGATGGCTATGACGGGCAACACAGGAGGC	489
Qy	530	CCCTAACTCGGATGGTGAAGGCTTTCTGAGTGCCTGGATGATCAAGAGGAGGAGGATGAGGA	589
Db	490	CCCGGACTCGGATGTTGAGGGCTACGTGA-----GGATGACGACGAGGAAGATGAGGA	543
Qy	590	TGAGGAGGAGTATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATGAGGA	649
Db	544	TGAGGAGGAGTATGATGAATATGCCAGCTAGTGGAAAGATGAAGAGGAAGAGGTTGAGGA	603
Qy	650	GGAGGAACGTGAAGAGGAGACGTGAGTGGAGACGAGGAGGAGAGGAGTGAAGGTTATAA	709
Db	604	GGAGAAGGGGGAAGAGAGATGTGAGTGGAGAGGAGGAGGAGATGAGGAAGGTTACAA	663
Qy	710	CAATGGAGAGGTAGATGATCAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCA	769
Db	664	TGACGGGGAAGTGGATGACGAGGAACAGNAGAAAGAGCTGGTGAAGAAGAAGGAGGTCA	723
Qy	770	GAACGAAAAATTAAGAACTGAAGATGAGGGAGAGAGCATGCCCTAAGTGGATATATCTAT	829
Db	724	GAACGAAAAAGCAACCGACGATGAGGGCGAAGAGGATGACTAAG-GAATGAACCTGT	782
Qy	830	TTTGAANAATTCCTTTTCTGATTTTACTGTTTTTACCGGTACCCCTCTCCCCCC	884
Db	783	TTGGGGAATTCCTATTGTGATTGACTGTTTTTACCCTATATCCCTCTCCCTCC	837

RESULT 15	
ABI99657	
ID	ABI99657 standard; cDNA; 980 BP.
XX	
AC	ABI99657;
XX	
DT	07-MAR-2002 (first entry)
XX	
DE	Mouse ischaemic condition related cDNA sequence SEQ ID NO:687.
XX	
KW	Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW	vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX	
OS	Mus musculus.
XX	
PN	WO200188188-A2.
XX	

PD	22-NOV-2001.	
XX		
PF	18-MAY-2001; 2001WO-JP04192.	
PR		
XX	18-MAY-2000; 2000JP-0145977.	
XX	(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.	
PA		
XX	Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;	
PI	WPI; 2002-034733/04.	
DR	P-PSDB; ABB57251.	
XX		
XX	Examining the ischemic condition (e.g. occlusive ischemia) by measuring	
PT	expression levels of particular genes defined in the specification or	
PT	by determining the expression profile of a gene group comprising these	
PT	genes -	
XX		
PS	Claim 2; Page 1714-1716; 2690pp; English.	
XX		
CC	The present invention describes a method for examining ischaemic	
CC	conditions, comprising measuring the expression levels of particular	
CC	genes (I) in a test sample or determining the expression profile of a	
CC	gene group in the sample comprising genes selected from (I). The method	
CC	is useful for examining the ischaemic condition (e.g. compressive	
CC	ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring	
CC	expression levels of particular genes (ABI99202 to ABI99912, encoding	
CC	the protein sequences in ABB57020 to ABB57374) or by determining the	
CC	expression profile of a gene group comprising these genes. The	
CC	expression levels or expression profiles produced by these genes are	
CC	used as an indicator when screening for ischaemic condition-improving	
CC	drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914	
CC	represent PCR primers for a mouse ischaemic condition related sequence,	
CC	which are used in the exemplification of the present invention.	
XX		
SO	Sequence 980 BP; 312 A; 169 C; 302 G; 197 T; 0 other;	

XX	Sequence	980 BP;	312 A;	169 C;	302 G;	197 T;	0 other;	
5Q	Query Match	64.5%;	Score 585;	DB 24;	Length 980;			
	Best Local Similarity	83.0%;	Pred. No. 1.6e-121;					
	Matches 693;	Conservative	0;	Mismatches 135;	Indels	7;	Gaps	
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QY	110	GCCTCTGATGTCAAGAAGACTTCTCTCTGGACACACGTGCGTTCGAATGAAGGCAAAATCGA	169					
DB	70	GCCTCTGATGTGAAGAGACTGCTCTGGATAACTCTAGTCAATTTGAAGGCAAAATCGA	129					
QY	170	AGGCTTCACAGATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAAGTAGAGCCCTCAC	239					
DB	130	AGGCTTCACGGATGAGTTTGAAGAACTGGAATTTCTTAAGTACAATCAAGTAGAGCCCTCAC	189					
QY	230	CTCAATCGCAAACTTACCAAGTTTAAACAACCTTGAAGACTTTGAACCTAGCAGTAAACAG	289					
DB	190	CTCCATTTCCAACCTTACCAAGTTTAAACAACCTTGAAGACTTTGAATTAAGCGAAACAG	249					
QY	290	AGCCTCAGTGGGCGCTAGAACGATTTGGCAGAAAAAGTGTCCAACACCTCATACATCTAAATTT	349					
DB	250	AACTCTAGGGGAGCTTGGAGTATTTGGCAGAGAATTTGCCGAACCTTAAAGCATCTAAATTT	309					
QY	350	AAGTGGCAACAAAAATTAAGACCTTCAGCACAATAGAGCGCCCTGAAAAGTTTGAAGAACCT	409					
DB	310	AAGTGGCAACAAAAATAAAGATCTCAGCACAATAGAGCGCTGAAAGAAAGTTAGAGAACT	369					
QY	410	CGAGAGCTTACGCTTTTTCATCTTGGAGGTAACCAACCTGAACAACTACTCTAGAGAGAT	469					
DB	370	CAAGAGCCTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCCTTACCGAGAAAACGT	429					
QY	470	GTTCAAGCTCCTCTGTCAACTCATATATCTCAACGGCTGTGACCCGGCTGACAAAGGAGGC	529					
DB	430	GTTCAAGCTCCTGTGCCCAAGGTGTATGCTACCTCGATGGCTATGACAGGAGCAACAGGAGGC	489					

Qy	530	CCCTAACTCGGATGGTCAGGGCTTTGTGGAGTCCTGGATGACAAGGAGGAGGATGAGGA	589
Db	490	CCCCGACTCCGATGTTGAGGGCTACGTGGA-----GGATGACGACGAGGAAGATCAGGA	543
Qy	590	TGAGGAGGAGTATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGA	649
Db	544	TGAGGAGGAGTATGATGAATATCCCGAGCTAGTGGAAAGATGAAGAGGAAGGTTGAGGA	603
Qy	650	GGAGGAACGTGAAGAGGAGGACGTGAGTGGAGACGAGGAGGAGAGGATGAAGGTTATAA	709
Db	604	GGAAGAAAGGGGAGGAGGAGGATGTGAGTGGAGGAGGAGGAGGATGAGGAAGGTTACAA	663
Qy	710	CAATGGAGAGGTAGATCAGCAGAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCA	769
Db	664	TGACGGGGAAGTGGATGACGAGGAGGAGACGAGAAAGCTGGTGAAGAAAGGAGGTCA	723
Qy	770	GAAGCGAAAAATAAGAACTGAAGATGAGGAGGAGAGACGATGCCTAAGTGAATATCTAT	829
Db	724	GAAGCGAAAAACGAGAACCGGACGATGAGGGCGAGAGGATGACTAAG-GAATGAACCTGT	782
Qy	830	TTTGAAAAATTCCTTTTGTCATTTTACTGTTTACTGTTTACCCGTAACCCCTCTCCCCCC	884
Db	783	TTGGGAAATTCCTATTGTGATTGACTGTTTATTACCCATATCCCTCCCTCCCTCC	837

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	825.4	91.0	1052	1 US-08-466-603-1	Sequence 1, Appli
2	825.4	91.0	1052	1 US-08-314-503A-1	Sequence 1, Appli
3	825.4	91.0	1052	1 US-08-468-066-1	Sequence 1, Appli
4	825.4	91.0	1052	2 US-08-466-717-1	Sequence 1, Appli
5	825.4	91.0	1052	1 US-08-466-743-1	Sequence 1, Appli
6	825.4	91.0	1052	5 PCT-US95-12414-1	Sequence 1, Appli
7	585	64.5	980	1 US-08-466-603-3	Sequence 3, Appli
8	585	64.5	980	1 US-08-314-503A-3	Sequence 3, Appli
9	585	64.5	980	1 US-08-468-066-3	Sequence 3, Appli
10	585	64.5	980	2 US-08-466-717-3	Sequence 3, Appli
11	585	64.5	980	3 US-08-466-743-3	Sequence 3, Appli
12	585	64.5	980	5 PCT-US95-12414-3	Sequence 3, Appli
13	405	44.7	759	1 US-08-466-603-4	Sequence 4, Appli
14	405	44.7	759	1 US-08-314-503A-4	Sequence 4, Appli
15	405	44.7	759	1 US-08-468-066-4	Sequence 4, Appli
16	405	44.7	759	2 US-08-466-717-4	Sequence 4, Appli
17	405	44.7	759	2 US-08-466-743-4	Sequence 4, Appli
18	405	44.7	759	5 PCT-US95-12414-4	Sequence 4, Appli
19	328.8	36.3	966	2 US-08-766-738-2	Sequence 2, Appli
20	328.8	36.3	966	4 US-09-262-610-2	Sequence 2, Appli
21	109.2	12.0	3489	2 US-08-728-323A-1	Sequence 1, Appli
22	109.2	12.0	3489	4 US-09-298-568-1	Sequence 1, Appli
23	109.2	12.0	32207	2 US-08-770-379-20	Sequence 20, Appl
24	109.2	12.0	32207	4 US-08-757-669A-20	Sequence 20, Appl
25	109.2	12.0	32207	4 US-09-230-371A-20	Sequence 20, Appl
26	107.6	11.9	7218	1 US-08-232-463-14	Sequence 14, Appl
27	104.6	11.5	16442	3 US-08-781-891-208	Sequence 208, App

C 28	99.8	11.0	1926	4	US-09-249-585A-4	Sequence 4, Appli
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35	80.4	8.9	390	4	US-09-197-649-7	Sequence 7, Appli
36	75.6	8.3	43795	3	US-08-742-185-101	Sequence 101, App
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39	73.4	8.1	2580	3	US-09-050-863-2	Sequence 2, Appli
40	73.4	8.1	2580	4	US-09-359-081-2	Sequence 2, Appli
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43	73.4	8.1	9600	4	US-09-620-925-1	Sequence 1, Appli
44	73.4	8.1	10596	1	US-07-884-811-15	Sequence 15, Appli
45	73.4	8.1	10596	1	US-07-885-971-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-466-603-1
; Sequence 1, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
US-08-466-603-1

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Query Match          91.0%; Score 825.4; DB 1; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCGAGAGAGAGAGCGC 60
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QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGGACGCCCTCTGTATG 120
Db 92 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGGACGCCCTCTGTATG 151
QY 121 TGAAGAAGCTTGCTCGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 180
Db 152 TGAAGAAGCTTGCTCGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 211
QY 181 ATGAATTTGAAGAACTCGAATTCCTTAAGTACAATCAAGTGAAGGCCCTCACAG 240
Db 212 ATGAATTTGAAGAACTCGAATTCCTTAAGTACAATCAAGTGAAGGCCCTCACAG 271
QY 241 ACTTACCAAGTTAAACAACTTAAAGAAGCTTGAAGCTAAGCAGTAACAGAGCCTCAGTGG 300
Db 272 ACTTACCAAGTTAAACAACTTAAAGAAGCTTGAAGCTAAGCAGTAACAGAGCCTCAGTGG 331
QY 301 GCCTAGAAGTATGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 332 GCCTAGAAGTATGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 391
QY 361 AAATTAAGACCTTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 420
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QY 421 ACCTTTTCACTTCGGAGGTAAACAACTGAAACACTGACAGAGAGATGTTCAAGCTCC 480
Db 452 ACCTTTTCACTTCGGAGGTAAACAACTGAAACACTGACAGAGAGATGTTCAAGCTCC 511
QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGATGACAGAGGAGGAGGAGGAGT 600
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RESULT 2
US-08-314-503A-1
; Sequence 1, Application US/08314503A
; Patent No. 5734022

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GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-314-503A-1
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Query Match          91.0%; Score 825.4; DB 1; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCGAGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGCGGGAGCCCTCGAGAGAGAGAGCGC 91
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QY 541 ATGGTGAGGGCTTTGGAGTGCCTGGATGACAAAGGAGGAGGAGGAGGAGGAGGAGT 631
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Db 512 TCCGCAACTCACATATCTGACGGCTATGACCGGACGACAAAGGAGGCCCTGACTCGG 571
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Db 752 TAGATGATGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 811
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 812 GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 871
QY 841 CCTTTTGTGATTTACTGTTTGTAGCGGTACCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCC 900
Db 872 CCTATTGTGATTTGACTGTTTGTACCATATCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCC 931
QY 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 3
US-08-468-066-1
; Sequence 1, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97...843
; US-08-468-066-1

Query Match 91.0%; Score 825.4; DB 1; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGGCTGGCGGGGAGCTCTGCGAGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGGCTGGCGGGGAGCTCTGCGAGAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGGACAGCGGATTCATTAGAGCTCGGAACGGGACGCCCTCTGATG 120
Db 92 GAGAGATGAGATGGGACAGCGGATTCATTAGAGCTCGGAACAGGAGCGCCCTCTGATG 151
QY 121 TGAAGAAGCTTGTCTGGACACAGTCGGTCGAANTGAGGGCAAACTCGAAGGCCCTCACAG 180
Db 152 TGAAGAAGCTTGTCTGGACACAGTCGGTCGAANTGAGGGCAAACTCGAAGGCCCTCACAG 211
QY 181 ATGAATTTGAAGAACTTGAATTTAAAGTACAATCAACGTAGGCGCTCACCTCAATCGCAA 240
Db 212 ATGAATTTGAAGAACTTGAATTTAAAGTACAATCAACGTAGGCGCTCACCTCAATCGCAA 271
QY 241 ACTTACCAAAAGTTAAACAACTTAAAGAGCTTGAACCTAAGCGGATACAGAGCCTCAGTGG 300
Db 272 ACTTACCAAAAGTTAAACAACTTAAAGAGCTTGAACCTAAGCGGATACAGAGCCTCAGTGG 331
QY 301 GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTATAATTTTAACTGGCAACA 360
Db 332 GCCTAGAAGTATTGGCAGAAAAAGTGTCCGCAACCTCAGCATCTAATTTTAACTGGCAACA 391
QY 361 AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAACTCTCGAGAGCTTAG 420
Db 392 AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAACTCTCAAGAGCTTAG 451
QY 421 ACCTTTTCACTTGGAGGTAAACCACTGACAACTACTGAGAGAGAGATGTTTCAAGCTCC 480
Db 452 ACCTTTTCACTTGGAGGTAAACCACTGACAACTACTGAGAGAGAGATGTTTCAAGCTCC 511
QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAACTCGG 540
Db 512 TCCCGCAACTCACATATCTCGACGGCTATGACCGGAGGAGGAGGAGGCCCTGACTCGG 571
QY 541 ATGCTGAGGGCTTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGAGT 600
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QY 661 AAGAGGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 692 AAGAGGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 751
QY 721 TAGATGATGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 752 TAGATGATGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 811
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Db 812 GAGAACCTGGAAGATGAGGAGAGATGACTAAGTGAATAACCTATTGAAAAATT 871
Qy 841 CTTTTGTGATTCTTTTGTAGCGGTACCCCTCTCCCGCCACACTCTAATCTGCC 900
Db 872 CCTATTGTGATTGACGTGTTTACCACATATCCCTCTCCCGCCCTCTAATCTGCC 931
Qy 901 CCCTGAA 907
Db 932 CCCTGAA 938
RESULT 4
US-08-466-717-1
; Sequence 1, Application US/08466717
; Patent No. 5874234
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.717
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
US-08-466-717-1
Query Match 91.0%; Score 825.4; DB 2; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
Qy 1 GGGTTCGGGGTTTATGATTGAATTGCGTCCGCGGAGCCCTCTCGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATGATTGAATTGCGTCCGCGGAGCCCTCTCGAGAGAGAGCGC 91
Qy 61 GAGAGATGGAGTGGGAGAGCGGATTCAATTTAGAGTGCAGGAGCGCCCTCTGTATG 120
Db 92 GAGAGATGGAGTGGGAGAGCGGATTCAATTTAGAGTGCAGGAGCGCCCTCTGTATG 151

Qy 121 TGAAGAACCTTGCTCTCGACAACACAGTCGGTCGAATGAAGCAAACTCGAAGCGCTCACAG 180
Db 152 TGAAGAACCTTGCTCTCGACAACACAGTCGGTCGAATGAAGCAAACTCGAAGCGCTCACAG 211
Qy 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACGTAGGCGCTCACCTCAATCGCAA 240
Db 212 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACGTAGGCGCTCACCTCAATCGCAA 271
Qy 241 ACTTACCAAAAGTTAAACAAAATTTAAGAAGCTTGAACCTAAGCAGTACACAGAGCTCAGTGG 300
Db 272 ACTTACCAAAAGTTAAACAAAATTTAAGAAGCTTGAACCTAAGCAGTACACAGAGTCTCAGGEG 331
Qy 301 GCCTAGAAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 332 GCCTAGAAAGTATTGGCAGAAAAGTGTCCAAACCTCACGACCTCAAGAGCTTAG 451
Qy 361 AAATTAAGAACCTTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 420
Db 392 AAATTAAGAACCTTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCAAGAGCTTAG 451
Qy 421 ACCTTTTCACTTCGAGGTTAACCAACCTGAACAACCTACTTGAGAGAGAGATGTTCAAGCTCC 480
Db 452 ACCTTTTCACTTCGAGGTTAACCAACCTGACGAGCTACCGAGAAAATGTTCAAGCTCC 511
Qy 481 TCCTGCAACTTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTTAACCTGG 540
Db 512 TCCTGCAACTTCACATATCTGACGGCTATGACCCGGAGCACAAGGAGGCCCTTAACCTGG 571
Qy 541 ATGGTGAGGCTTGTGAGTGCCTGGATGACAAGGAGGAGATGAGGATGAGGAGGT 600
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Qy 601 ATGATCAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGTG 660
Db 632 ATGATCAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGTG 691
Qy 661 AAGAGGAGGAGTGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 692 AAGAGGAGGAGTGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 751
Qy 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 752 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 811
Qy 781 AAGAAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 812 GAGAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 871
Qy 841 CCTTTTGTGATTTTACTGTTTTTACCGGTACCCCTCTCCCGCCCACTCTAATCTCTGCC 900
Db 872 CCTATTGTGATTTGACTGTTTTTACCCATATCCCTCTCCCGCCCACTCTAATCTCTGCC 931
Qy 901 CCCTGAA 907
Db 932 CCCTGAA 938
RESULT 5
US-08-466-743-1
; Sequence 1, Application US/08466743
; Patent No. 6040173
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia

Query Match	91.0%;	Score	825.4;	DB	3;	Length	1052;
Best Local Similarity	94.4%;	Pred. No.	1.7e-187;				
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Gaps	0;						
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Db	32	GGGTTCCGGGGTTTATTGATTGAATTCGGCTCGCGCGGAGCCTCTGCAGAGAGAGAGCGC	91				
Qy	61	GAGAGATGGAGATGGGCAGACGGATTATTTAGAGCTTGGGAGCGGACGCCCTCTGTGAT	120				
Db	92	GAGAGATGGAGATGGGCAGACGGATTATTTAGAGCTTGGGAGCGGACGCCCTCTGTGAT	151				
Qy	121	TGAAGAAGACTTGCCTGGCAACACGTCCGTGCGAATGAAGGCAAACTCGAAGGCGCTCACAG	180				
Db	152	TGAAGAAGACTTGCCTGGCAACACGTCCGTGCGAATGAAGGCAAACTCGAAGGCGCTCACAG	211				
Qy	181	ATGAATTTGAAGAAGCTTGGAAATCTTTAAGTACAATCAACGTAGGCGCTCACCTCAATCGCAA	240				
Db	212	ATGAATTTGAAGAAGCTTGGAAATCTTTAAGTACAATCAACGTAGGCGCTCACCTCAATCGCAA	271				
Qy	241	ACTTACCAAGTTAAACAACCTTAGAAGCTTGAACCTTAAGCAGTAACAGAGCGCTCAGTGG	300				
Db	272	ACTTACCAAGTTAAACAACCTTAGAAGCTTGAACCTTAAGCAGTAACAGAGCTCCTCAGGGG	331				
Qy	301	GCCTAGAAGTATTGGCAGAAAAGTGTCGCAAACTCATACATCTAAATTTAAGTGGCAACA	360				
Db	332	GCCTAGAAGTATTGGCAGAAAAGTGTCGCAAACTCACGCATCTAAATTTAAGTGGCAACA	391				
Qy	361	AAATTAAGACCTCAGACACAATAGAGCCCTGTGAAAAGTTAGAAAACCTCGAGAGCTTAG	420				
Db	392	AAATTAAGACCTCAGACACAATAGAGCCCTGTGAAAAGTTAGAAAACCTCAAGAGCTTAG	451				
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Db	452	ACCTTTTCAATTCGGAGGTAAACCAACTGACGACTCCGAGAAAATGTGTTCAAGCTCC	511				
Qy	481	TCCTGCAACTCACATATCTCAACGGGTGTGACCCGGATGACAAGGAGGCCCTTAACTCGG	540				

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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97...843
PCT-US95-12414-1

Query Match 91.0%; Score 825.4; DB 5; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTCGGGGTTATGATGAATTCGGCTGGCGGGGAGCCTCTGCGAGAGAGAGCGC 60
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QY 32 GGGTCGGGGTTATGATGAATTCGGCTGGCGGGGAGCCTCTGCGAGAGAGAGCGC 91
Db |||||
QY 61 GAGAGATGAGATGGCAGACGAGTTCATTTAGAGCTCGGAAAGGAGCGCCTCTGATG 120
Db |||||
QY 92 GAGAGATGAGATGGCAGACGAGTTCATTTAGAGCTCGGAAAGGAGCGCCTCTGATG 151
Db |||||
QY 121 TGAAGAAGCTTCTCTGGACACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCTTCACAG 180
Db |||||
QY 152 TGAAGAAGCTTCTCTGGACACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCTTCACAG 211
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QY 181 ATGAATTTCAAGAACTGGAATTTTAAGTACAACTAGGCTACCTCAATTCGCA 240
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QY 392 AAATTAAGAGCTCAGCAATAGAGCCCTGAAAGTTAGAAAACCTCAAGAGCTTAG 451
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QY 421 ACCTTTTCACTTGGAGGTAACCAACCTGAAACACTACTGAGAGAAGATGTTCAAGCTCC 480
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QY 452 ACCTTTTCAATTTGGAGGTAACCAACCTGAAACACTACTGAGAGAAGATGTTCAAGCTCC 511
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QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGATGACAGAGAGGCCCTTAACCTCG 540
Db |||||
QY 512 TCCCGCAACTCACATATCTCAACGGCTGTGACCGGATGACAGAGAGGCCCTTAACCTCG 571
Db |||||
QY 541 ATGCTGAGGGCTTTGTGAGTGCCTGGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600
Db |||||
QY 572 ATGCTGAGGGCTACGTGGAGGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631
Db |||||
QY 601 ATGATGAAGATGCTCAGGTAAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db |||||
QY 632 ATGATGAAGATGCTCAGGTAGTGAAGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 691
Db |||||
QY 661 AAGAGGAGGAGCTCAGTGGACACAGAGAGAGAGGATGAAGGTTATAACAATGAGAGAGG 720
Db |||||
QY 692 AAGAGGAGGAGCTCAGTGGAGGAGGAGGAGGATGAAGGTTATAACAATGAGAGAGG 751
Db |||||
QY 721 TAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTCAAGAGCGAAAT 780
Db |||||
QY 752 TAGATGAGGAGAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTCAAGAGCGAAAT 811
Db |||||
QY 781 AAGAACTGAAGATGAGGAGAGAGAGATGCCTTAAGTGAATATCTATTTTGAAGAAAT 840
Db |||||
QY 812 GAGAAGCTGAAGATGAGGAGAGAGATGATGACTAAGTGAATACCTATTTTGAAGAAAT 871
Db |||||
QY 841 CCTTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCCCTCACTCTAATCTGCGC 900
Db |||||
QY 872 CCTATTGTGATTTGACTGTTTTTACCATATCCCTCTCCCCCTCACTCTAATCTGCGC 931
Db |||||
QY 901 CCCTGAA 907
Db |||||

Db 932 CCCTGAA 938

RESULT 7

US-08-466-603-3
; Sequence 3, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,603
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: mus sp
US-08-466-603-3

Query Match 64.5%; Score 585; DB 1; Length 980;
Best Local Similarity 83.0%; Pred. No. 2.5e-130;
Matches 693; Conservative 0; Mismatches 135; Indels 7; Gaps 2;

QY 50 AGAGAGAGCGGAGAGATGGAGATGGCAGACGGATTCATTTAGAGCTGCGGAAGCGGAC 109
Db |||||
QY 110 GCCCTCTGATGTGAAGAAGTCTCTCGTGGACAAACAGTCGCTCAATGAAGCAAACTCGA 169
Db |||||
QY 170 AGGCCTCACAGATGAATTTGAAGAAGTCTTAACTCACTCAACAGTAGGCCTCAC 229
Db |||||
QY 230 CTCATTCGCAAACTTACCAAAAGTTAAACAAACTTAAAGAGCTTGAACAGTGAACAG 289
Db |||||
QY 290 AGCCTCAGTGGGCTTAGAGATTTGCGAGAAAAGTGTCCAAACCTCATACATCTAAATTT 349
Db |||||
QY 250 AATCTCAGGGACCTTGGAGATTTGGCAGAGAAATGTCCGAAACCTTAAAGCATCTAAATTT 309

QY 350 AAGTGGCAACAAATTAAGACCTCAGCAATAGAGCCCTGAAAAAGTTAGAAACCT 409
Db 310 AAGTGGCAACAAATTAAGACCTCAGCAATAGAGCCCTGAAAAAGTTAGAAACCT 369
QY 410 CGAGAGCTTAGACCTTTTCACTTCGAGGTAAACCAACCTGAAACAACTACTGAGAGAAGT 469
Db 370 CAAGAGCTTAGACCTTTTCACTTCGAGGTAAACCAACCTGAAACAACTACTGAGAGAAGT 429
QY 470 GTTCAAGCTCCTCTGCAACTCATATCTCAACGGCTGTGACCGGATCACAAGGAGGC 529
Db 430 GTTCAAGCTCCTCTGCAACTCATATCTCAACGGCTGTGACCGGATCACAAGGAGGC 489
QY 530 CCTCAACTCGATGTGAGGCTTTGTGAGTGCCTGATGACAAAGGAGGAGGATGAGGA 589
Db 490 CCCGACTCCGATGTTGAGGCTAGTGGA-----GGATGACGACGAGGAAGATGAGGA 543
QY 590 TGAGGAGGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGA 649
Db 544 TGAGGAGGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGA 603
QY 650 GGAGGAGCTGAAGGAGGAGGAGTGTGAGTGGAGGAGGAGGAGGAGGAGGAGGATGAGGA 709
Db 604 GGAAGAGGAGGAGGAGGAGTGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGATGAGGA 663
QY 710 CAATGAGGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGA 769
Db 664 TGAGGAGGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGA 723
QY 830 TTTGAAAAATTCCTTTTGTGATTTACTGTTTGTAGCCGTACCCCTCTCCCCC 884
Db 783 TTGGGNAATTCCTTTTGTGATTTACTGTTTGTAGCCGTACCCCTCTCCCCC 837

RESULT 8
US-08-314-503A-3
; Sequence 3, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: mus sp
US-08-314-503A-3

Query Match 64.5%; Score 585; DB 1; Length 980;
Best Local Similarity 83.0%; Pred. No. 2.5e-130;
Matches 693; Conservative 0; Mismatches 135; Indels 7; Gaps 2;

QY 50 AGAGAGCGCGAGAGATGGGAGATGGGAGACGGATTCAITTTAGAGCTGCGGAACGGGAC 109
Db 10 AGAGAGCGCGAGAGATGGGAGATGGGAGACGGATTCAITTTAGAGCTGCGGAACGGGAC 69
QY 110 GCCCTCTGATGTGAAAGAACTTGTCTGGACAACAGTCGGTGCAGTGAAGGCAAACTCGA 169
Db 70 GCCCTCTGATGTGAAAGAGCTGGTCTGGATAACTGAAGTCAATTAAGGCAAACTCGA 129
QY 170 AGGCTCAGAGATGAATTTGAAGAAGTCTTAAAGAACTTAAAGAACTTGAAGTCAATTAAGGCAAACTCGA 229
Db 130 AGGCTCAGAGATGAATTTGAAGAAGTCTTAAAGAACTTAAAGAACTTGAAGTCAATTAAGGCAAACTCGA 189
QY 230 CTCAATCGCAAACTTTACCAAAAGTAAACAAAGTAAAGAACTTGAAGTCAATTAAGGCAAACTCGA 289
Db 190 CTCAATCGCAAACTTTACCAAAAGTAAACAAAGTAAAGAACTTGAAGTCAATTAAGGCAAACTCGA 249
QY 290 AGGCTCAGTGGGCTTGAAGATTTGGGAGAAAGTGTCCAAACCTCATACATCTAAATTT 349
Db 250 AATCTCAGGAGCTTGAAGATTTGGGAGAAAGTGTCCAAACCTCATACATCTAAATTT 309
QY 350 AAGTGGCAACAAATTAAGACCTCAGCAATAGAGCCCTGAAAAAGTTAGAAACCT 409
Db 310 AAGTGGCAACAAATTAAGACCTCAGCAATAGAGCCCTGAAAAAGTTAGAAACCT 369
QY 410 CGAGAGCTTAGACCTTTTCACTTCGAGGTAAACCAACCTGAAACAACTACTGAGAGAAGT 469
Db 370 CAAGAGCTTAGACCTTTTCACTTCGAGGTAAACCAACCTGAAACAACTACTGAGAGAAGT 429
QY 470 GTTCAAGCTCCTCTGCAACTCATATCTCAACGGCTGTGACCGGATGACAAGGAGGC 529
Db 430 GTTCAAGCTCCTCTGCAACTCATATCTCAACGGCTGTGACCGGATGACAAGGAGGC 489
QY 530 CCTCAACTCGATGTGAGGCTTTGTGAGTGCCTGATGACCTGCTATGACAGGAGCAACAAGGAGGC 589
Db 490 CCCGACTCCGATGTTGAGGCTAGTGGA-----GGATGACGACGAGGAAGATGAGGA 543
QY 590 TGAGGAGGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGA 649
Db 544 TGAGGAGGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGA 603
QY 650 GGAGGAGCTGAAGGAGGAGGAGTGTGAGTGGAGGAGGAGGAGGAGGAGGATGAGGA 709
Db 604 GGAAGAGGAGGAGGAGGAGTGTGAGTGGAGGAGGAGGAGGAGGAGGATGAGGA 663
QY 710 CAATGAGGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGA 769
Db 664 TGAGGAGGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGA 723
QY 770 GAAAGGAAATTAAGAACTGAAGATGAGGAGGAGGAGGAGGAGGATGAGGA 829
Db 724 GAAAGGAAATTAAGAACTGAAGATGAGGAGGAGGAGGAGGAGGATGAGGA 782

RESULT 9
US-08-468-066-3
; Sequence 3, Application US/08468066

```

: Patent No. 5756676
:
: GENERAL INFORMATION:
: APPLICANT: Pasternack, Gary R.
: APPLICANT: Kuhajda, Francis P.
: TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
: TITLE OF INVENTION: Uncontrolled Cell Division
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner, Birch, McKie & Beckett
: STREET: 1001 G Street, N.W.
: CITY: Washington, D.C.
: STATE: District of Columbia
: COUNTRY: U.S.A.
: ZIP: 20001
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468,066
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/314,503
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Posorske Esq., Laurence H.
: REGISTRATION NUMBER: 34,698
: REFERENCE/DOCKET NUMBER: 1107.47218
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202 508-9153
: TELEFAX: 202 508-9299
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 980 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cdna
: ORIGINAL SOURCE:
: ORGANISM: mus sp
:
: US-08-468-066-3
:
: Query Match 64.5%; Score 585; DB 1; Length 980;
: Best Local Similarity 83.0%; Pred. No. 2.5e-130;
: Matches 699; Conservative 0; Mismatches 135; Indels 7; Gaps 2;
:
: QY 50 AGAGAGCGCGAGAGATGGAGATGGCGACAGCGATTATTAGAGCTCGCGAAGCGGAC 109
: DB 10 AGAGAGCGCGAGAGATGGAGATGGCGACAGCGATTATTATTAGAGCTCGCGAAGCGGAC 69
: QY 110 GCCCTCTGATGTGAAGAACTTCTCTGGACACAGCTCGGTGCAATGAAGCAAACTCGA 169
: DB 70 GCCCTCTGATGTGAAGAGCTGCTCTGGATACACTGTAAGTCAATTGAAGCAAAATCGA 129
: QY 170 AGGCCTCACAGATGAATTTGAAGAACTGGAATTTCTTAAGTCAAACTCAAGCTAGCGCTCAC 229
: DB 130 AGGCCTCACAGATGAGTTTGAAGAACTGGAATTTCTTAAGTCAAACTCAAGCTAGCGCTCAC 189
: QY 230 CTCATCCGAACTTACCAAGTTTAAACAACTTAAGAGCTTGAACCTAAGCAGTAACAG 289
: DB 190 CTCATTTCCAACTTACCAAGTTTAAACAACTTAAGAGCTTGAATTAAGCGAAACAG 249
: QY 290 AGCCTCAGTGGGCTAGAAGTATTGGCAGAAAAGTGTCCAACTCTACATCTAAATTT 349
: DB 250 AATCTCAGGGACCTGGAAGTATTGGCAGAAAAGTGTCCGAACTCTAAGCATCTAAATTT 309
: QY 350 AAGTGGCAACAATAAAGACTCAGCAATAGAGCCCTGAAAAGTTAGAAAACCT 409
: DB 310 AAGTGGCAACAATAAAGACTCAGCAATAGAGCCCTGAAAAGTTAGAGAATCT 369
: QY 410 CGAGAGCTTAGACCTTTTACCTTGGCGAGTAAACCAACCTGAACAACTACTCAGAGAAGAT 469

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: mus sp
US-08-466-717-3

Query Match 64.5%; Score 585; DB 2; Length 980;
Best Local Similarity 83.0%; Pred. No. 2.5e-130;
Matches 693; Conservative 0; Mismatches 135; Indels 7; Gaps 2;

QY 50 AGAGAGAGCGGAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTCGGAGCGGAC 109
DB 10 AGAGAGAGCGGAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTCGGAGCGGAC 69

QY 110 GCCCTCTGATGGAAGAACTTTCCTGGCAACAGTCGGTTCGAATGAAGCGCAAACTCGA 169
DB 70 GCCCTCTGATGGAAGAACTTTCCTGGCAACAGTCGGTTCGAATGAAGCGCAAACTCGA 129

QY 170 AGGCCTCAGATGAATTTGAAGAACTTTCGAATTCGAATTCGAATTCGAATTCGAATTC 229
DB 130 AGGCCTCAGATGAATTTGAAGAACTTTCGAATTCGAATTCGAATTCGAATTCGAATTC 189

QY 230 CTCATTCGCAAACTTACCAAGTTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACT 289
DB 190 CTCATTCGCAAACTTACCAAGTTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACT 249

QY 290 AGCCTCAGTGGCCCTAGAGTATTTGGGAGAGAAAGTTCCTCAACCTCATCATCTAAATTT 349
DB 250 AATCTCAGGAGCCTGGAAGTATTTGGGAGAGAAAGTTCCTCAACCTCATCATCTAAATTT 309

QY 350 AAGTGGCAACAAATTAAGAACTTTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTT 409
DB 310 AAGTGGCAACAAATTAAGAACTTTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTT 369

QY 410 CGAGAGCTTAGACCTTTTCACTTGGAGTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACT 469
DB 370 CAAGAGCTTAGACCTTTTCACTTGGAGTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACT 429

QY 470 GTTCAAGCTCCTCCTCAACTACATATCTCAACGGCTGTGACCCGGATGACAGGAGGC 529
DB 430 GTTCAAGCTCCTCCTCCTCAACTACATATCTCAACGGCTGTGACCCGGATGACAGGAGGC 489

QY 530 CCTCACTCGAGTGGTGGGCTTTTGGAGTGCCTGGAGTGCCTGGAGTGCCTGGAGTGCCTGGAG 589
DB 490 CCTCACTCGAGTGGTGGGCTTTTGGAGTGCCTGGAGTGCCTGGAGTGCCTGGAGTGCCTGGAG 543

QY 590 TGAGGAGGAGTATGATGAAGATGCTCAGGTATGGAAGATGGAAGATGGAAGATGGAAGATGGA 649
DB 544 TGAGGAGGAGTATGATGAAGATGCTCAGGTATGGAAGATGGAAGATGGAAGATGGAAGATGGA 603

QY 650 GGAGGAGGAGTATGATGAAGATGCTCAGGTATGGAAGATGGAAGATGGAAGATGGAAGATGGA 709
DB 604 GGAGGAGGAGTATGATGAAGATGCTCAGGTATGGAAGATGGAAGATGGAAGATGGAAGATGGA 663

QY 710 CAATGGAGGAGTATGATGAAGATGCTCAGGTATGGAAGATGGAAGATGGAAGATGGAAGATGGA 769
DB 664 TGAGGAGGAGTATGATGAAGATGCTCAGGTATGGAAGATGGAAGATGGAAGATGGAAGATGGA 723

QY 770 GAAGCGAAATTAAGAACTTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 829
DB 724 GAAGCGAAATTAAGAACTTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782

QY 830 TTTGAAATTCCTTTTGTGATTTTACTGTTTGTAGCCGTTTGTAGCCGTTTGTAGCCGTTTGTAGCC 884
DB 783 TTTGAAATTCCTTTTGTGATTTTACTGTTTGTAGCCGTTTGTAGCCGTTTGTAGCCGTTTGTAGCC 837

RESULT 11
US-08-466-743-3
; Sequence 3, Application US/08466743
; Patent No. 6040173
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.

APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated with
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,743
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: mus sp
US-08-466-743-3

Query Match 64.5%; Score 585; DB 3; Length 980;
Best Local Similarity 83.0%; Pred. No. 2.5e-130;
Matches 693; Conservative 0; Mismatches 135; Indels 7; Gaps 2;

QY 50 AGAGAGAGCGGAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTCGGAGCGGAC 109
DB 10 AGAGAGAGCGGAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTCGGAGCGGAC 69

QY 110 GCCCTCTGATGGAAGAACTTTCCTGGCAACAGTCGGTTCGAATGAAGCGCAAACTCGA 169
DB 70 GCCCTCTGATGGAAGAACTTTCCTGGCAACAGTCGGTTCGAATGAAGCGCAAACTCGA 129

QY 170 AGGCCTCAGATGAATTTGAAGAACTTTCGAATTCGAATTCGAATTCGAATTCGAATTC 229
DB 130 AGGCCTCAGATGAATTTGAAGAACTTTCGAATTCGAATTCGAATTCGAATTCGAATTC 189

QY 230 CTCATTCGCAAACTTACCAAGTTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACT 289
DB 190 CTCATTCGCAAACTTACCAAGTTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACT 249

QY 290 AGCCTCAGTGGCCCTAGAGTATTTGGGAGAGAAAGTTCCTCAACCTCATCATCTAAATTT 349
DB 250 AATCTCAGGAGCCTGGAAGTATTTGGGAGAGAAAGTTCCTCAACCTCATCATCTAAATTT 309

QY 350 AAGTGGCAACAAATTAAGAACTTTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTT 409
DB 310 AAGTGGCAACAAATTAAGAACTTTCGAATTCGAATTCGAATTCGAATTCGAATTCGAATTT 369

QY 410 CGAGAGCTTAGACCTTTTCACTTGGAGTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACT 469
DB 370 CAAGAGCTTAGACCTTTTCACTTGGAGTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACT 429

CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466.603
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE: Mus sp
FEATURE:
NAME/KEY: CDS
LOCATION: 3..548
US-08-466-603-4

Query Match 44.7%; Score 405; DB 1; Length 759;
Best Local Similarity 80.4%; Pred. No. 1.5e-87;
Matches 501; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

Qy 262 TTAAGAAGCTTGAACCTAAGCAGTAAACAGAGCCCTCAGTGGCCCTAGAGTATTGGCAGAAA 321
Db 4 TCAAGAAGCTTGAATTAAGCGAAACAGAACTCTCAGGGGACCTGGAAGTATTGGCAGAGA 63

Qy 322 AGTGTCACAACTCATACATCTAAATTTAAGTGGCAACAAATTAAGAGCTCTCAGCACAA 381
Db 64 AATGTCGGAACCTTAAGCATCTAAATTTAAGTGGCAACAAATTAAGAGCTCTCAGCACAA 123

Qy 382 TAGAGCCCTGAAAGAGTTAGAAACCTCGAGAGCTTAGACCTTTTTCACATTCGCGAGTAA 441
Db 124 TAGAGCCCTGAAAGAGTTAGAGATCTCAAGAGCTTAGACCTTTTTCACATTCGCGAGTAA 183

Qy 442 CCAACCTGAACAACTACTGAGAGAGAGATGTTCAAGCTCTCCTCGCACTACATATCTCA 501
Db 184 CCAACCTGAATGCTTACCGAGAAACGTTTCAAGCTCTCCTCGCACTACATATCTCA 243

Qy 502 ACGGCTGTGACCCGATGACAGAGAGCCCTCACTCGGATGGTGGGGCTTTGTGGAGT 561
Db 244 ATGGCTATGACAGGAGCAACAGAGGAGGCCCCCGACTCGGATGTTGAGGGCTACGTGA-- 301

Qy 562 GCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATCAAGATGCTCAGTAA 621
Db 302 ---GGATGACGACGAGGAGGATGAGGATGAGGAGGAGTATGATCAATATGCCAGCTAG 357

Qy 622 TGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681
Db 358 TGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417

Qy 682 ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 741

Db 418 AGAGGAGGAGGAGTGAAGAGGTTTACATGACGGGAGTGGATGACGAGGAAGACGAG 477
Qy 742 AAGAGCTTGGTGAAGAAGAAGGGTTCAGAGCGAAATTAAGAACTGAAGATGAGGAG 801
Db 478 AAGAAGCTGGTGAAGAAGAAGGGTTCAGAGCGAAATTAAGAACTGAAGATGAGGAG 537
Qy 802 AAGAGGATGCTTGAAGTGAATATCTATTTGAAATAATCTCTTTGTGATTTACTGTTT 861
Db 538 AAGAGGATGACTAAG-GAATGAACCTGTTTGGGGAATTTCTTATTTGATTTGACTGTTT 596
Qy 862 TTAGCCGTACCCCTCTCCCTCC 884
Db 597 TTACCATATCCCTCCCTCC 619

RESULT 14
US-08-314-503A-4
Sequence 4, Application US/08314503A
Patent No. 5734022
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kujada, Francis P.
TITLE OF INVENTION: NO. 5734022el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE: Mus sp
FEATURE:
NAME/KEY: CDS
LOCATION: 3..548
US-08-314-503A-4

Query Match 44.7%; Score 405; DB 1; Length 759;
Best Local Similarity 80.4%; Pred. No. 1.5e-87;
Matches 501; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

Qy 262 TTAAGAAGCTTGAACCTAAGCAGTAAACAGAGCCCTCAGTGGCCCTAGAGTATTGGCAGAAA 321
Db 4 TCAAGAAGCTTGAATTAAGCGAAACAGAACTCTCAGGGGACCTGGAAGTATTGGCAGAGA 63

Qy 322 AGTGTCACAACTCATACATCTAAATTTAAGTGGCAACAAATTAAGAGCTCTCAGCACAA 381

Db 64 AATGCCGACCTTAAAGATCTAAATTTAAGTGGCAACAAAATAAAGATCTCAGCACAA 123
QY 382 TAGAGCCCTGAAAAGCTTAGAAAACCTCGAGAGCTTTAGACCTTTTACCTTGGCAGGTAA 441
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QY 442 CCAACCTGAACTACTCTAGAGAGATGTTCAAGCTTCTCCCTGCAACTCACATATCTCA 501
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QY 502 ACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAACCTCGGATGCTGAGGCTTTGTGGAGT 561
Db 244 ATGCTATGACAGGACCAACAGAGAGGCCCTCCGACTCCGATGTTGAGGGCTAGCTGGA-- 301
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QY 622 TGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681
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QY 682 ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 741
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QY 802 AAGAGCTTGTGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 861
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Db 597 TTACCATATCCCTCCCTCCCTCC 619

RESULT 15

US-08-468-066-4

; Sequence 4, Application US/08468066

; Patent No. 5756676

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kujajda, Francis P.

; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated with

; TITLE OF INVENTION: Uncontrolled Cell Division

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Banner, Birch, McKie & Beckett

; STREET: 1001 G Street, N.W.

; CITY: Washington, D.C.

; STATE: District of Columbia

; COUNTRY: U.S.A.

; ZIP: 20001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,066

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/314,503

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Posorske Esq., Laurence H.

; REGISTRATION NUMBER: 34,698

; REFERENCE/DOCKET NUMBER: 1107.47218

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9153

; TELEFAX: 202 508-9299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 759 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Mus sp

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 3..548

US-08-468-066-4

Query Match

Best Local Similarity 44.7%; Score 405; DB 1; Length 759;

Matches 501; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

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Db 4 TCAGAAGCTTGAATTAAGCGAAACAGAACTCAGGGGACCTGGAAGTATTGGCAGAGA 63

QY 322 AGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAAATTTAAAGACCTCAGCACAA 381

Db 64 AATGTCCGAACCTTAAGCATCTAAATTTAAGTGGCAACAAAATTTAAAGATCTCAGCACAA 123

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QY 502 ACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAACCTCGGATGTTGAGGGCTTTGTGGAGT 561

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QY 562 GCCTGGATGACAGGAGGAGGATGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 621

Db 302 ----GGATGACGAGGAGGAGGATGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357

QY 622 TGGAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681

Db 358 TGGAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417

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Db 538 AAGAGGATGACTAAG--GAATGAACCTGTTTGGGGAATTCCTATTCTGATTGACATGTTT 596

QY 862 TTAGCCGTACCCCTCTCCCTCC 884

Db 597 TTACCATATCCCTCCCTCCCTCC 619

Search completed: December 8, 2002, 23:19:39

Job time : 43.3808 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 22:43:58 ; Search time 41.4109 Seconds
(without alignments)
8540.478 Million cell updates/sec

Title: US-09-591-500-4

Perfect score: 907

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications.NA.*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	217.8	24.0	718	10	US-09-910-943-76
2	215.4	23.7	771	10	US-09-910-943-166
3	214	23.6	748	10	US-09-910-943-132
4	188.4	20.8	763	10	US-09-910-943-622
5	124.6	13.7	557	9	US-10-046-935-2145
6	124.6	13.7	557	9	US-09-878-178-2145
7	119.8	13.2	720	9	US-10-101-487-74
8	119.8	13.2	720	9	US-10-101-487-76
9	117.4	12.9	554	9	US-10-101-487-69
10	117.4	12.9	554	9	US-10-101-487-106
11	115.6	12.7	522	9	US-10-101-487-71
12	115.6	12.7	522	9	US-10-101-487-73
13	106	11.7	575	10	US-09-864-761-20733
14	106	11.7	1969	10	US-09-864-761-3972
15	101	11.1	659158	9	US-09-771-208-20
16	91.8	10.1	423	10	US-09-864-761-18355
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18	91.4	10.1	3809	12	US-10-001-870-68
19	89.8	9.9	474	10	US-09-864-761-11284

c	20	89.6	9.9	267	10	US-09-864-761-27984	Sequence 27984, A
c	21	89.4	9.9	344	10	US-09-864-761-19694	Sequence 19694, A
c	22	89.4	9.9	700	10	US-09-864-761-17529	Sequence 17529, A
c	23	85.4	9.4	1944	10	US-09-864-761-2825	Sequence 2825, Ap
c	24	85	9.4	53226	10	US-09-818-264-3	Sequence 3, Appl
c	25	83.2	9.2	350	10	US-09-822-263-19	Sequence 19, Appl
c	26	83.2	9.2	381	10	US-09-777-564-700	Sequence 700, App
c	27	83.2	9.2	399	10	US-09-864-761-2913	Sequence 2913, Ap
c	28	82	9.0	5387	9	US-10-001-873-22	Sequence 22, Appl
c	29	81.8	9.0	583	10	US-09-864-761-20772	Sequence 20772, A
c	30	81.8	9.0	1959	10	US-09-864-761-4012	Sequence 4012, Ap
c	31	81.6	9.0	299	10	US-09-864-761-21553	Sequence 21553, A
c	32	81.6	9.0	345	10	US-09-822-263-17	Sequence 17, Appl
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c	37	80	8.8	497	10	US-09-822-263-35	Sequence 35, Appl
c	38	80	8.8	766	10	US-09-864-761-19608	Sequence 19608, A
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c	42	78.4	8.6	251	10	US-09-864-761-19674	Sequence 19674, A
c	43	78.2	8.6	276	10	US-09-864-761-20595	Sequence 20595, A
c	44	77.8	8.6	465	10	US-09-864-761-23120	Sequence 23120, A
c	45	77.6	8.6	305	10	US-09-864-761-19262	Sequence 19262, A

ALIGNMENTS

RESULT 1

US-09-910-943-76
; Sequence 76, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/IG148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(718)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-76

Query Match 24.0%; Score 217.8; DB 10; Length 718;
Best Local Similarity 61.8%; Pred. No. 5.1e-42;
Matches 364; Conservative 0; Mismatches 222; Indels 3; Gaps 1;

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QY	124	AAGAATTGCTTGGACACAGTCGGTTCGAATGAAGCAACTCGAAGGCTCACAGATG	183
Db	192	AAGAATTGGTCTTAGATAACTGCCGTTTCAGACGATGCAAAATTTATTGGACTGACCTCAG	251
QY	184	AATTGAAGAACTGGATTCTTAAGTACATCAACTAGGCGCTCACCTCAATCGCAACT	243
Db	252	AGTTTGAAGCCCTGGAGTTTCTCAGCATGATAAATTCACACTTATTATCTGTAGCTAACT	311
QY	244	TAGCAAGTTTAAACAACACTTGAAGCTTGAACCTAAGACAGTAAACAGAGGCTCAGTGGGC	303
Db	312	TGCCAAGACTCCCAAGTTGAAAAGCTGCAACTCAGTGACATCGAATCGAATCTCTGTGGAGAT	371

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Db 492 TCTTTAACTGTGAGTGACCATGCTAAACAACCTACAGGAGAGTGTTTTGAATCTTCC 551
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QY 484 TGCAACTCATATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTCAACTCGGATG 543
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QY 544 GTGAGGCTTTGTGAGTGCCTGGATGACAAAGGAGGAGATGAGATGAGGAGGATG 603
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RESULT 2

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US-09-910-943-166
; Sequence 166, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/IG148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 166
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(771)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-166
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Query Match 23.7%; Score 215.4; DB 10; Length 771;
Best Local Similarity 62.0%; Pred. No. 1.9e-41;
Matches 375; Conservative 0; Mismatches 223; Indels 7; Gaps 2;
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QY 124 AAGAACTTGTCTCGGACAACAGTCGGTGAATGAAGGCAAACTCGAAGGCCCTCAGAGATG 183
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Db 213 AAGAATTGTTCTAGATAACTGCCGTTTCAGACGATGGCAAAATATTGGACTGACCTCAG 272
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QY 184 AATTTGAGAAGTGAATCTTTAAGTACAACTCAAGGTAGGCCCTCACCTCAATCGCAAACT 243
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Db 273 AGTTTGAAGCCTGGAGTTTCTCAGCATGATAAATGTCAACTTATTATCTGTAGCTAACT 332
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QY 244 TACCAAGTTAAACAACTTTAAGAGCTTGAAGCTTAAGCAGTAACAGAGCCTCAGTGGGCC 303
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QY 424 TTTTCACTTGGAGGTAACCAACCTGAACAACCTACTGTAGAGAAGATGTTCAACCTCTCC 483
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Db 750 GAAAA 754
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RESULT 3

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; Sequence 132, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/IG148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 132
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(748)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-132
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Query Match 23.8%; Score 214; DB 10; Length 748;
Best Local Similarity 61.7%; Pred. No. 4e-41;
Matches 359; Conservative 0; Mismatches 220; Indels 3; Gaps 1;
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Qy 424 TTTTCACTTGGGAGTAACCAACCTGAACAACTACTTGAGAGAGAGATGTTCAAGCTCTCTCC 483
Db 492 TCFTTAACTGTGAGGTGACCATGCTTAACAACACTACAGGAGAGAGTGTTTTGAACTTCTCC 551
Qy 484 TGCACACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGAGGCCCTTAACCTCGATG 543
Db 552 CTAAGCTTACCTTTTGTAGATGTTTGTGTCAGATGACCAAGAGGCTCCAGATTTCTGATC 611
Qy 544 GTGAGGCTTTGTGAGTGCCTGGATGACAAGAGAGAGATGAGATGAGGAGGATG 603
Db 612 CAGAGG---CTGAAGATTTAGAGGAAATGGAGAGATGTTGAGGAGGATGAAGAAGATG 668
Qy 604 ATGAAGATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATG 645
Db 669 ATGAAGAGAAGAAGAAATTGAAGATGAGCTTGATGATGAGG 710

RESULT 4
US-09-910-943-622
; Sequence 622, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/IG148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 622
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(763)
; OTHER INFORMATION: n may be a or g or c or t/u

US-09-910-943-622

Query Match 20.88; Score 188.4; DB 10; Length 763;
Best Local Similarity 60.28; Pred. No. 4e-35;
Matches 342; Conservative 0; Mismatches 222; Indels 4; Gaps 2;

Qy 64 AGATGGAGATGGGACGCGGATTCATTTAGAGCTGCGGAACGGGACGCCCTCTGATGTA 123
Db 134 ACATGGACATGAAAAGAGATTGATGCTGGAGCTCAGGAATCGGAAAGCGGCTGACGCTA 193
Qy 124 AAGAATCTGCTGGACAACAGTCGGTCAATGAAGCAACTCGAAGGCTCAGATG 183
Db 194 AAGAATGGTCTAGATAACTGCCGTTTCAGACGATGCGCAAAATATTGGATGACCTCAG 253
Qy 184 RAATTTGAAGAACTGGAATCTTAAGTACAATCAACGTAGGCGCTCACCTCAATCGCAAACT 243
Db 254 AGTTTGAAGCCTGGAGTTTCTCAGCATGATTAATGTCAACTTATATCTGTAGCTAACT 313
Qy 244 TACCAAGATTAAACAACTTAAGAAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGGGCC 303
Db 314 TGCCAAAGCTCCCAAGTTGAAAAGCTGGAACCTCAGTGACAACTCTCTGGAGGAT 373
Qy 304 TAGAAGTATTGCCAAGAAAGTGTCCAAACCTCAVACATCTAAATTTAAGTGGCAACAAA 363
Db 374 TAGAGGTAAGTGCAGCAAGGACCCCAAAATTTGACACACTGAACCTCAGTGGGACAGA 433
Qy 364 TTAAGACCTCAGCACAATAGAGCCCTGAAAAGCTTAGAAAACCTCGAGAGCTTAGACC 423
Db 434 TAAAGAGATAAATACCTTAGAGCCACITTAAGAAACTACCTCATCTCATGATCTGGACC 493
Qy 424 TTTTCACTTGGAGGTAAACCAACTGACAACACTACTTGAGAGAGATGTTCAAGCTCTCTCC 483
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Db 494 TCTTTAACTGTGAGGTGACCATGCTAAACAACACTACAGGAGAGTGTTTTTTGAACCTTCTCC 553
Qy 484 TGCACACTCACATATCTCAACGGCTGTGACCGGATGACAAGGAGGCCCTTAACCTCGATG 543
Db 554 T-AAGCTTACCTTTTGTAGATGTTTGTATGCANATGACCAGGANGCTCCAGATTTCTGATC 612
Qy 544 GTGAGGCTTTGTGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGATG 603
Db 613 CAGAG---CTGAAGAAATTNAGGAAATGGAGAGATGTTGAGAGGATGAANAATG 669
Qy 604 ATGAAGATGCTCAGGTAATGGAAGATGA 631
Db 670 TGAAGAAGAAGAAGAAATTTGGAAGATGA 697

RESULT 5
US-10-046-935-2145
; Sequence 2145, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2145
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-046-935-2145

Query Match 13.7%; Score 124.6; DB 9; Length 557;
Best Local Similarity 57.3%; Pred. No. 2.9e-20;
Matches 248; Conservative 0; Mismatches 179; Indels 6; Gaps 1;

Qy 378 ACAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGAGCTTTAGACCTTTTCACTTCCGAG 437
Db 1 ACAGTAGAAGCTCTGCAAAATCTTAAAAATTTGAAAAGTCTTGACCTGTTTAACTGTGAG 60
Qy 438 GTAACCAACCTGAACACTACTAGAGAGATGTTTCAAGCTCCTCTGCAACTCACATAT 497
Db 61 ATCACAACCTGGAAGATTATAGAGAAAGTATTTTGAAGTACTGAGCAATCACATAC 120
Qy 498 CTCACGGCTGTGACCCGGATGACAAGGAGGCCCTTAACCTCGGATGGTGAGGGCTTTGTG 557
Db 121 TTAGATGGATTTTCATCAGGAGGATAATGAAGCCCGGACTCTGAGAGGAGGATGATGAG 180
Qy 558 GAGTGCTGTGATGACAAGAGGAGGATGAGGATGAGGAGGAGTAT----GATGAAGAT 611
Db 181 GATGGCATGAAGATGATGAAGAGGAGGAAGAAATGAAGCTGGTCCACCGGAGGATAT 240
Qy 612 GCTCAGTAATGGAAGATGAGGAGGAGGATGAGGATGAGGAGGAGGATGATGATGATGAT 671
Db 241 GAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGATGAGGATGAGGATGAAGATGAAGATGA 300
Qy 672 GTGAGTGGAGCAGGAGGAGGAGGATGAAGGTTTAAACAATGGAGAGGTAGATGATGAG 731
Db 301 CGAGGTTTCAGAGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 732 GAAGATGAAGAGAGCTTTGTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 791
Db 361 GAAATTCAGGATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 792 GATGAGGAGAGAG 804
Db 421 GAGGAAGAGGAG 433
```

RESULT 6
US-09-878-178-2145
; Sequence 2145, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secret, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2145
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-2145

Query Match 13.7%; Score 124.6; DB 9; Length 557;
Best Local Similarity 57.3%; Pred. No. 2.9e-20;
Matches 248; Conservative 0; Mismatches 179; Indels 6; Gaps 1;
QY 378 ACAATAGAGCCCTGAAAAAGTTAGAAACCTCGAGAGCTTACACCTTTTCACTTCGCGAG 437
DB 1 ACAGTAGAAGCTCTGCAAAATCTTAAATTTTCAAAAGCTTGACCTGTTTAACTCTGAG 60
QY 438 GTRACCAACCTGACACACTACTGAGAGAGATGTTCAAGCTCCTCTGCAACTACATAT 497
DB 61 ATCAAAACCTGGAAGATTATAGAGAAAGTATTTTGAACCTACTGACGCAAAATCACATAC 120
QY 498 CTCAACGGCTGTGACCCGGATGACAGGAGGCCCTTAACTCGATGGTGAGGCTTTTGG 557
DB 121 TTAGATGGATTGTCAGGAGGATATGAGCCCGGACTCTGAGAGGAGGATGATGAG 180
QY 558 GAGTGCCGTGATGACAGAGGAGGAGGATGAGGATGAGGAGGAGTAT-----GATGAAGAT 611
DB 181 GATGGCGATGAAGATGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 612 GCTCAGGTAATGAAGATGAGGAGGAGGAGGATGAGGATGAGGAGGAGGAGGAGGAGGAGGAG 671
DB 241 GAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 672 GTGAGTGGAGACGAGGAGGAGGAGGATGAGGTTTATAACAATGGAGAGGTAGATGATGAG 731
DB 301 GCAGGTTTCAGAGTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 732 GAAGATGAAGAGAGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 791
DB 361 GAAATTCAGATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 792 GATGAGGAGAG 804
DB 421 GAGGAGAGAGGAG 433

RESULT 7
US-10-101-487-74
; Sequence 74, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(718)
US-10-101-487-74

Query Match 13.2%; Score 119.8; DB 9; Length 720;
Best Local Similarity 61.3%; Pred. No. 4.3e-19;
Matches 193; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
QY 510 GACCCGGATGACAGGAGGAGCCCTTAACCTCGGATGCTGAGGCTTTGTGGAGTGCCTGGAT 569
DB 374 GAAGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 433
QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 629
DB 434 GAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 494 GNAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 553
QY 690 GAGAAGGATGAAGGTTATACATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGAT 749
DB 554 GAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 613
QY 750 GGTGAAGAGAGAGGGGTGACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 809
DB 614 GAAGAG 673
QY 810 GCCTAAGTGAATAA 824
DB 674 GAGGAAGAGGAGGAA 688

RESULT 8
US-10-101-487-76/c
; Sequence 76, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-101-487-76

Query Match 13.2%; Score 119.8; DB 9; Length 720;
Best Local Similarity 61.3%; Pred. No. 4.3e-19;
Matches 193; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAGGAGGCCCTTAACTCGGATGGTGGAGCTTTGTGGAGTGCTCGAT 569
DB 351 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 292
QY 570 GACAAAGGAGGAGGATGAGGATGAGGAGGATGATGATGAAGATGCTCAGGTTAATGGAAGAT 629
DB 291 GAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 232
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 231 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 172
QY 690 GAGAAGGATGAAGTTTATAACAATGGAGGATGATGATGATGATGATGATGATGATGAT 749
DB 171 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 112
QY 750 GGTGAAGAGAAAGGGGTGAGAGCGAAATTAAGAACTGAAGATGAGGAGGAGGAGGAT 809
DB 111 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 52
QY 810 GCCTAAGTGAATAA 824
DB 51 GAGGAAGAGGAGGAA 37

RESULT 9
US-10-101-487-69
; Sequence 69, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(528)
US-10-101-487-69

Query Match 12.9%; Score 117.4; DB 9; Length 554;
Best Local Similarity 60.5%; Pred. No. 1.4e-18;
Matches 193; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAGGAGGCCCTTAACTCGGATGGTGGAGCTTTGTGGAGTGCTCGAT 569
DB 229 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 288

QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGATGATGATGAAGATGCTCAGTGAATGAAGAT 629
DB 289 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 589
DB 349 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 408
QY 690 GAGAAGATGAAGTTTATACANTGGAGGAGGATGATGATGATGATGATGATGATGATGAT 749
DB 409 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468
QY 750 GGTGAAGAGAAAGGGTCAAGAGCGAAATTAAGAACTGAAGATGAGGAGGAGGAGGAT 809
DB 469 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 528
QY 810 GCCTAAGTGAATAA 828
DB 529 GAAGAGGAGGAGTCTTCTA 547

RESULT 10
US-10-101-487-106
; Sequence 106, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(537)
US-10-101-487-106

Query Match 12.9%; Score 117.4; DB 9; Length 554;
Best Local Similarity 60.5%; Pred. No. 1.4e-18;
Matches 193; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAGGAGGCCCTTAACTCGGATGGTGGAGCTTTGTGGAGTGCTCGAT 569
DB 229 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 288
QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGATGATGATGAAGATGCTCAGTGAATGAAGAT 629
DB 289 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 349 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 408
QY 690 GAGAAGATGAAGTTTATACAAATGGAGGAGGATGATGATGATGATGATGATGATGATGAT 749
DB 409 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468

QY 750 GGTGAAGAAAGGGGTGAGAACCGAAATAAGAACTGAAGATGAGGAGAGACGAT 809
DB 469 GAAGAGGAAGAGAGGAGGAAGAGAGGAGGAAGAGAGGAGAGAGAGAGAG 528
QY 810 GCCTAAGTGGATATCTA 828
DB 529 GAAGAGGAGTAGTCTTCTA 547

RESULT 11
US-10-101-487-71
; Sequence 71, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; US-10-101-487-71

Query Match 12.7%; Score 115.6; DB 9; Length 522;
Best Local Similarity 60.5%; Pred. No. 3.6e-18;
Matches 190; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAAGAGGCCCTTAACTCGGATGCTGAGGCTTTGTGGAGTGCCTGGAT 569
DB 127 GAAGAGGAAGAGAGGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAATGGAAGAT 629
DB 187 GAAGAGGAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
DB 247 GAAGAGGAAGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
QY 690 GAGAAGGATGAAGCTTATAACAATGGAGAGGTAGATGATGAGGAGGAGGAGGAGCTT 749
DB 307 GAAGAGGAAGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366
QY 750 GGTGAAGAAAGGGGTGAGAACCGGAAATAAGAACTGAAGATGAGGAGAGACGAT 809
DB 367 GAAGAGGAAGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
QY 810 GCCTAAGTGGATA 823
DB 427 GAAGAGGAAGA 440

RESULT 12
US-10-101-487-73/c
; Sequence 73, Application US/10101487

; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; US-10-101-487-73

Query Match 12.7%; Score 115.6; DB 9; Length 530;
Best Local Similarity 60.5%; Pred. No. 3.7e-18;
Matches 190; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAAGAGGCCCTTAACTCGGATGCTGAGGCTTTGTGGAGTGCCTGGAT 569
DB 404 GAAGAGGAAGAGAGGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345
QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAATGGAAGAT 629
DB 344 GAAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCTT 749
DB 284 GAAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
QY 690 GAGAAGGATGAAGCTTATAACAATGGAGGCTAGATGATGAGGAGGAGGAGGAGCTT 749
DB 224 GAAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 165
QY 750 GGTGAAGAAAGGGGTGAGAACCGGAAATAAGAACTGAAGATGAGGAGAGACGAT 809
DB 164 GAAGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 105
QY 810 GCCTAAGTGGATA 823
DB 104 GAAGAGGAAGA 91

RESULT 13
US-09-864-761-20733
; Sequence 20733, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26


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; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20733
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005822.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
; OTHER INFORMATION: EST_HUMAN HIT: BE071749.1, EVALUAE 5.80e+00
;
US-09-864-761-20733
Query Match 11.7%; Score 106; DB 10; Length 575;
Best Local Similarity 61.0%; Pred. No. 6.7e-16;
Matches 172; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 515 GGATGACAAAGGAGCCCTACTCGGATGGTGAGGGCTTTGTGGAGTGCCTGGATGACAA 574
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Db 254 GGAGGAGAAAGAAAGAGGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 313
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Db 374 GGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 433
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Qy 695 GGATGAAGGTTATACAAATGAGAGAGGTAGATGATGAGAGACATGAAGAGAGCTTGTGTA 754
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Db 434 GGAAGAGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 493
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QY 755 AGAAGAAAGGGTCTCAGAAGCGAAATAAGAACTCAAGATGA 796
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DB 494 AGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGA 535

RESULT 14
US-09-864-761-3972
; Sequence 3972, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3972
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005822.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 11
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:26:48 ; Search time 1333.73 Seconds
(without alignments)
11013.667 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em.estba:*
2: em.esthum:*
3: em.estnu:*
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7: em.estc:*
8: em.estf:*
9: gb.est1:*
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12: gb.est3:*
13: gb.est4:*
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27: em.gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	776.4	85.6	1034	AL518839	AL518839
2	773.8	85.3	894	AL533191	AL533191
3	770.2	84.9	923	AL560249	AL560249
4	769.8	84.9	875	AL535686	AL535686
5	756.6	83.4	870	AL537874	AL537874
6	753.8	83.1	875	AL547157	AL547157

7	753.6	83.1	903	9	AL540827	AL540827
8	738	81.4	1035	14	BM904155	BM904155
9	731.2	80.6	855	9	AL543743	AL543743
10	728	80.3	992	9	AL517375	AL517375
11	716.2	79.0	834	9	AL545880	AL545880
12	716.2	79.0	853	9	AL535863	AL535863
13	710.8	78.4	895	14	BQ232856	BQ232856
14	706	77.8	1066	13	BM543218	BM543218
15	698.4	77.0	894	9	AL571434	AL571434
16	696	76.7	802	9	AL518247	AL518247
17	679.2	74.9	999	13	BM460209	BM460209
18	679	74.9	806	9	AL547462	AL547462
19	672	74.1	749	13	BI860951	BI860951
20	668.2	73.7	961	13	BM475803	BM475803
21	665.6	73.4	866	14	BQ687251	BQ687251
22	662.2	73.0	775	12	BF969229	BF969229
23	660.2	72.8	882	14	BQ427516	BQ427516
24	651.2	71.8	902	9	AL516007	AL516007
25	645.6	71.2	899	14	BQ890554	BQ890554
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27	641.6	70.7	859	14	BQ212622	BQ212622
28	641	70.7	764	12	BG323551	BG323551
29	640	70.6	1004	13	BM469555	BM469555
30	624.4	68.8	737	9	AL122593	AL122593
31	616.6	68.0	710	9	AL557479	AL557479
32	613	67.6	697	9	AU123726	AU123726
33	608.8	67.1	764	10	BE561138	BE561138
34	608	67.0	683	10	BE544189	BE544189
35	606	66.8	790	10	BE409600	BE409600
36	602	66.4	850	14	BQ229967	BQ229967
37	601.4	66.3	1141	11	AK020753	AK020753
38	599.4	66.1	988	14	BQ216493	BQ216493
39	595	65.6	762	10	BE561131	BE561131
40	593.2	65.4	728	10	AU130628	AU130628
41	592	65.3	652	9	AL535685	AL535685
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ALIGNMENTS

RESULT 1	AL518839	AL518839	1034 bp	mRNA	linear	EST 13-FEB-2001
LOCUS	AL518839	LTI_NFL011_NBC1	Homo sapiens	cDNA	clone	CS0DA011YH23 5
DEFINITION	AL518839	prime, mRNA sequence.				
ACCESSION	AL518839	AL518839.1	GI:12782332			
VERSION	AL518839	EST.				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
REFERENCE	1 (bases 1 to 1034)					
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Pollayes,D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage Bp 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.					
FEATURES	Location/Qualifiers					
source	1.1034					
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	/db_xref="taxon:9606"					
	/clone="CS0DA011YH23"					
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	/sex="male"					
	/tissue.type="neuroblastoma cells"					
	/lab_host="DH10B"					

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 317 a 190 c 300 g 223 t 4 others
ORIGIN

Query Match 85.6%; Score 776.4; DB 9; Length 1034;
Best Local Similarity 93.4%; Pred. No. 8.5e-161;
Matches 807; Conservative 3; Mismatches 54; Indels 0; Gaps 0;

QY 44 CTGCAGAGAGAGCGCGAGAGATGGAGATGGGACGCGATTTCATTTAGAGCTGCGGAA 103
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Db 1 CTGCAGAGAGAGCGCGAGAGATGGAGATGGGACGCGATTTCATTTAGAGCTGCGGAA 60
QY 104 CGGACGCGCTCTGATGTGAAGAACTTGTCTGGACACAGTCGGTCGAATGAAGCAA 163
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Db 61 CAGGACGCCCTCTGATGTGAAGAACTTGTCTGGACACAGTCGGTCGAATGAAGCAA 120
QY 164 ACTCGAAGCGCTCACAGATGAATTTGAAGAACTGTGAATTCCTTAAGTACAATCAACGTAGG 223
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Db 121 ACTCGAAGCGCTCACAGATGAATTTGAAGAACTGTGAATTCCTTAAGTACAATCAACGTAGG 180
QY 224 CCTCACCCTCAATCGCAACTTACCAAGTTAAACAATTTAAGAACTTGAACCTTAAGCAG 283
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Db 181 COTCACCCTCAATCGCAACTTACCAAGTTAAACAATTTAAGAACTTGAACCTTAAGCAG 240
QY 284 TAACGAGCCTCAGTGGCGCTAGAGTATTGCGAGAAAGTGTCACAACTCATACATCT 343
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Db 241 TAACGAGCTCAGGGGCCCTGGAGATTTGCGAGAAAGTGTCCGAACCTTCACGCATCT 300
QY 344 AAATTTAAGTGGCAACAAATTAAGAGCCTCAGCACATAGAGCCCTGAAAGATTTAGA 403
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Db 301 AAATTTAAGTGGCAACAAATTAAGAGCCTCAGCACATAGAGCCCTGAAAGATTTAGA 360
QY 404 AAACCTCAGAGCTTAGACCTTTTCACCTTGGAGGTATACCACTGAACACTACTGAGA 463
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Db 361 AAACCTCAGAGCTTAGACCTTTTCACCTTGGAGGTATACCACTGAACACTACTGAGA 420
QY 464 GAAGATGTTCAAGCTCCCTCCCTGCAACTCACATATCTCAACGGCTGTGACCGGATGACAA 523
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Db 421 AAATGTTTCAAGCTCTCCCGCAACTCACATATCTGACGGCTATGACCGGACGACAA 480
QY 524 GGAGCCCTTAACCTGGATGTGAGGGCTTTGTGAGTGGCTGGATGACAAAGGAGGAGGA 583
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Db 481 GGAGCCCTTAACCTGGATGTGAGGGCTTTGTGAGTGGCTGGATGAGGAGGAGGA 540
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Db 781 ACCATTTTGAATAATCTCTTTTGTGATTTGACCTGTTTGTGTTTGTGTTTGTGTTTGTG 840
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QY 884 CCACTCTAATCTGCCCCCTGAA 907
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Db 841 CACCTCCAATCTGCCCTGAA 864

RESULT 2
AL533191

LOCUS AL533191 LRI_FL015_Brn1 Homo sapiens cDNA clone CSODN003YK10 5
DEFINITION Prime, mRNA sequence.
ACCESSION AL533191 894 bp mRNA linear EST 13-FEB-2001
VERSION AL533191.1 GI:12796684
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 894)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Source

1. 894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODN003YK10"
/clone_lib="LRI_FL015_Brn1"
/sex="male"
/tissue_type="Adult brain"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 293 a 159 c 270 g 170 t 2 others
ORIGIN

Query Match 85.3%; Score 773.8; DB 9; Length 894;
Best Local Similarity 94.2%; Pred. No. 3.2e-160;
Matches 813; Conservative 1; Mismatches 48; Indels 1; Gaps 1;

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QY 61 GAGAGATGAGATGGCAGACGCGATTTCATTAGAGCTGCGGAACGGGACGCCCTCTGTATG 120
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Db 91 GAGAGATGAGATGGCAGACGCGATTTCATTAGAGCTGCGGAACGAGGACGCCCTCTGTATG 150
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Db 151 TGAAGAACCTTGTCTTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 210
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Db 271 ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAACCTTAAGCAAGTAAACAGAGCTCAGGSG 330
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Qy 421 ACCTTTTCACTTGGAGGTAACA-ACCTGAACAACCTACTGAGAGAGATGTTCAAGCTC 479
Db 451 ACCTTTTCAATTTGGAGGTAACCAACCTGAACGACTACCGAGAAATGTTTCAAGCTC 510
Qy 480 CTCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTTAAGTCG 539
Db 511 CTCCTGCAACTCACATATCTCGAGGCTATGACCGGGACGACAAGGAGGCCCTGACTCG 570
Qy 540 GATGTGTAGGGCTTTGTGGAGTGCCTCGATGACAAGGAGGAGGATGAGGATGAGGAGG 599
Db 571 GATGTGTAGGGCTACGTTGGAGGCTCGATGAGGAGGAGGATGAGGATGAGGAGGAG 630
Qy 600 TATGATGAAGATGCTCAGGTAATGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAG 659
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Qy 660 GAAAGAGGAGGCTGAGTGGAGGAGGAGGAGGAGGAGGATGAAGTTTATACATGAGAG 719
Db 691 GAAAGAGGAGGCTGAGTGGAGGAGGAGGAGGAGGAGGATGAAGTTTATACATGAGAG 750
Qy 720 GTAGATGATGAGGAGATGAAGAGAGGCTGTGAGAGAGAGAGGCTGAGAGGAGGAGG 779
Db 751 GTAGATGAGGAGGAGATGAAGAGAGGCTGTGAGAGAGAGAGGCTGAGAGGAGGAGG 810
Qy 780 TAAGAACTGAAGATGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGATGAGGAGGAG 839
Db 811 CGAGAACCTGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGATGAGGAGGAGG 870
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Db 871 TCCTATTGTGATTTGACTGTTTT 893

RESULT 3
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LOCUS AL560249 LTI_FL011_BCl Homo sapiens cDNA clone CS0DG002YI23 5 prime
DEFINITION , mRNA sequence.
ACCESSION AL560249
VERSION AL560249.1 GI:12906528
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 923)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/lab_host="DH10B"
/note="vector: PCWSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-stranded cDNA was digested with Not I and cloned
into the Not I and Eco RV sites of the PCWSPORT 6 vector.
Library was constructed by Life Technologies. Contact :
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BASE COUNT 299 a 163 c 279 g 175 t 7 others
ORIGIN
Query Match 84.9%; Score 770.2; DB 9; Length 923;
Best Local Similarity 93.5%; Pred. No. 2e-159;
Matches 807; Conservative 6; Mismatches 49; Indels 1; Gaps 1;
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Qy 61 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGGAGCCCTCTGATG 120
Db 122 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGGAGCCCTCTGATG 181
Qy 121 TGAAGAAGACTTCTCTGGACAAACAGTCGGTCGAATGAAGCAAACTCGAAGGCTCACAG 180
Db 182 TGAAGAAGACTTCTCTGGACAAACAGTCGGTCGAATGAAGCAAACTCGAAGGCTCACAG 241
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Db 722 AAGAGGAGGAGTGTGAGTGGAGAGGAGGAGGAGGAGGATGAAGTTTAAACAATGGAGAG 781
Qy 721 TAGATGATGAGGAGATGAAGAGAGCTTCGTGAAGAAGAGAGGCTCAGAAGCGGAGAAAT 780
Db 782 TAGATGAGGAGGAGATGAAGAGAGCTTCGTGAAGAAGAGAGGCTCAGAAGCGGAGAAAT 841
Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGATGCCTTAAGTGAATTAATCTATTTTCAAAAAT 840
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Qy 841 CCTTTTGTGATTTTACTGTTTT 863
Db 902 -CYATTGTGATTTGACTGTTTT 923
RESULT 4
```

Feng Liang Life Technologies, a division of Invitrogen
9800 Medical Center Drive Rockville, Maryland 20850, USA
Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

```

AL535686
LOCUS AL535686 875 bp mRNA linear EST 13-FEB-2001
DEFINITION AL535686 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF016YA23 5
prime, mRNA sequence.
ACCESSION AL535686
VERSION AL535686.1 GI:12799179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 291 a 156 c 267 g 160 t 1 others
ORIGIN
Query Match 84.9%; Score 769.8; DB 9; Length 875;
Best Local Similarity 94.4%; Pred. No. 2.4e-159;
Matches 798; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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QY 61 GAGAGATGAGATGGCAGACGGATTTCATTAGAGCTCGCGAAGCGGAGCCCTCTGATG 120
DB 91 GAGAGATGAGATGGCAGACGGATTTCATTAGAGCTCGCGAAGCGGAGCCCTCTGATG 150
QY 121 TGAAGAAGACTTGCTCGACACAGTCGGTCGAATGAAGCGAACTCGAAGGCGCTCACAG 180
DB 151 TGAAGAAGACTTGCTCGACACAGTCGGTCGAATGAAGCGAACTCGAAGGCGCTCACAG 210
QY 181 ATGAATTTGAAGAAGCTGGAATTCCTTAAGTACAATCAACGTAGCGCTCACTCAATCGCAA 240
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QY 301 GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
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DB 511 TCCCGCAACTCACATATCTGACGGCTATGACCGGGACACAAAGAGGCGCCCTGACTCGG 570
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QY 601 ATGATGAAGATGCTCAGGTAAATCGAAGATGAGGAGGAGGAGGAGGAGGAGGAGG 660
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QY 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
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prime, mRNA sequence.
ACCESSION AL537874
VERSION AL537874.1 GI:12801367
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 290 a 156 c 265 g 155 t 4 others

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Db 690 AAGAGGACGACGTGAGTGAGGAGGAGGAGGAGGAGGATCAAGAGGTTATACGATGAGGAGG 749
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QY 721 TAGATGATGAGGAAGATGAAGAGGCTTGGTGAAGAGAAAGGGTCCAGAGCCAAAT 780
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LOCUS , mRNA sequence. EST 16-FEB-2001
DEFINITION AL540827
ACCESSION AL540827
VERSION AL540827.1 GI:12871345
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Li W.B., Gruber C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 298 a 160 c 271 g 164 t 10 others
ORIGIN

Query Match 83.1%; Score 753.6; DB 9; Length 903;
Best Local Similarity 93.1%; Pred. No. 8.9e-156;
Matches 788; Conservative 9; Mismatches 48; Indels 1; Gaps 1;

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Db 112 GARAAAGGAGAGGAGGACGAGGATTCATTTAGAGCTCGGGAACGGGACGCCCTCTGATG 171
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ACCESSION BM904155
VERSION BM904155.1 GI:19354489
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgi.mgi.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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cdna Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12133 row: d column: 11
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Average insert size 1.867 kb. Library enriched for
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Note: this is a NIH_MGC Library."
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 855)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 280 a 151 c 265 g 152 t
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Query Match 80.6%; Score 731.2; DB 9; Length 855;
Best Local Similarity 94.0%; Pred. No. 7.7e-151;
Matches 754; Conservative 5; Mismatches 43; Indels 0; Gaps 0;
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DEFINITION prime, mRNA sequence.
ACCESSION AL517375
VERSION AL517375.1 GI:12780868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 992)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 992

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/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life technologies. Contact : Feng Liang Life technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 301 a 174 c 289 g 217 t 11 others
ORIGIN

Query Match 80.3%; Score 728; DB 9; Length 992;
Best Local Similarity 91.9%; Pred. No. 3.8e-150;
Matches 772; Conservative 7; Mismatches 59; Indels 2; Gaps 1;

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QY 548 GGGCTTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGA 607
Db 481 GGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGTATGATGA 540
QY 608 AGATGCTCAGGTAATGGAAGATCAGGAGGACGAGGATGAGGAGGAGGAGGAGGAGGAGGAG 667
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QY 668 GGACGTTCAGTGGAGCAGGAGGAGGAGGATGAAGGTTTATAACAATGGAGAGTAGATGA 727
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LOCUS
DEFINITION AL545880 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1023YE09 5
prime, mRNA sequence.
ACCESSION AL545880
VERSION
KEYWORDS EST.
SOURCE
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 834)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/clone_lib="LTI_NFL006.PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 272 a 153 c 257 g 148 t 4 others
ORIGIN
Query Match 79.0%; Score 716.2; DB 9; Length 834;
Best Local Similarity 94.1%; Pred. No. 1.5e-147;
Matches 739; Conservative 4; Mismatches 42; Indels 0; Gaps 0;
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Db 645 ATGATGAAGATGCTCAGGTAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGAACTG 704
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Qy 661 AAGAGGAGGAGCTGAGTGGAGACGAGGAGGAGGATGAAGGTTATAAATCGAGAGG 720
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Qy 781 AAGAA 785
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prime, mRNA sequence.
ACCESSION AL535863
VERSION AL535863.1 GI:12799356
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 853)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 283 a 147 c 254 g 164 t 5 others
ORIGIN
Query Match 79.0%; Score 716.2; DB 9; Length 853;
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Best Local Similarity 92.08; Pred. No. 1.5e-147;		Matches 785; Conservative 4; Mismatches 57; Indels 7; Gaps 3;	
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Qy	257	CAAACTTTAAGAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGGGCTAGAAGTATTGGC	316
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Qy	317	AGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAATTAAGACCTCAG	376
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Qy	377	CACAAATAGGCGCTGAAAAGTTAGAAAACCTCGAGAGCTTAGACCTTTTCACTTGGCA	436
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Qy	610	ATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGACGTTGAAGAGGAGG	669
Db	601	ATGCTCAGGTAGTGAAGACGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG	660
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Qy	790	AAGATGAGGAGGAGGAGGAGGCTTAACTGGAATTAATCTATTTTGAAGAACTTCTTTGTG	849
Db	781	AAGATGAGGAGGAGGAGGAGGCTTAACTGGAATTAATCTATTTTGAAGAACTTCTTTGTG	840
Qy	850	ATTTTACTGTGTTT 862	
Db	841	ATTTGACTGTTT 853	

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5', mRNA sequence.
ACCESSION B0232856
VERSION B0232856.1 GI:20414256
KEYWORDS EST.
SOURCE human.

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REFERENCE 1 (bases 1 to 895)		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue procurement: DCTD/DTP/Gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13328 row: n column: 12 High quality sequence stop: 676.			
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		/lab_host="DH10B (phage-resistant)"	
		/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."	
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	QY	661	AAGAGGAGGACTGAGTGGAGACGAGGAGAGAAGCATGAAGGTTATAACAATGGAGAGG	720
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	QY	721	TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAA-CAAAGGGGTCAGAAGCGAAAA	779
	Dd	766	TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAACAAAGGGGTCAGAAGCGAAAA	825
	QY	780	TAAGAA-CTGAAGATGA-CGGAGAACACCATGCCCTAAGTGG----ATAATCTATTITG	833
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	DEFINITION	5', mRNA sequence.		
	ACCESSION	BM5433218		
	VERSION	BM5433218.1 GI:18773420		
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	SOURCE	human.		
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	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	AUTHORS	NIH-MGC http://mgi.nci.nih.gov/		
	TITLE	1 (bases 1 to 1066)		
	JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
	COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Found through the MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12327 row: b column: 18 High quality sequence stop: 628.		
	FEATURES	Location/Qualifiers		
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	Query Match	77.8%	Score 706;	DB 13; Length 1066;
	Best Local Similarity	92.4%	Pred. No. 2.6e+145;	
	Matches 787; Conservative	0; Mismatches 60; Indels 5; Gaps 4;		
	QY	60	CGAGAGATGGAGTGGGCAGACGATTCATTTAGAGCTGCGGAACGGACGCCCTCTGAT	119

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. .894
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 177 a 266 c 165 g 279 t 7 others
ORIGIN

Query Match 77.0%; Score 698.4; DB 9; Length 894;
Best Local Similarity 92.3%; Pred. No. 1.3e-143;
Matches 742; Conservative 4; Mismatches 55; Indels 3; Gaps 1;
QY 107 GAGCGCCCTCTGATGTGAAGAACTTGCTCTGACAAACAGTCGGTGAATGAAGCAAACT 166
DB 891 GAGCGCCCTCTGATGTGAAGAACTTGCTCTGACAAACAGTCGGTGAATGAAGCAAACT 832
QY 167 CGAAGGCCCTCAGATGAATTTGAAGAACTTGAATTTCTTAAGTACAATCAACGTAGGCCT 226
DB 831 CGAAGGCCCTCAGATGAATTTGAAGAACTTGAATTTCTTAAGTACAATCAACGTAGGCCT 772
QY 227 CACCTCAATCGCAAACTTTACCAAACTTTAAACAACTTAAAGAACTTGAACCTAAGCAGTAA 286
DB 771 CACCTCAATCGCAAACTTTACCAAACTTTAAACAACTTAAAGAACTTGAACCTAAGCAGTAA 712
QY 287 CAGAGCCCTCAGTGGCCCTAGAGTAATGGCAGAAAAGTGTCCAAACCTCATACATCTAAA 346
DB 711 CAGAGCTCAGGGGCCCTGGAAGTATTGGCAGAAAAGTGTCCGAACTCAGGCATCTAAA 652
QY 347 TTTAAGTGGCACAAATTAAGACCTCAGCACATAGAGCCCTGAAAAGTTAGAAA 406
DB 651 TTTAAGTGGCACAAATTAAGACCTCAGCACATAGAGCCCTGAAAAGTTAGAAA 592
QY 407 CCTCGAGAGCTTAGACCTTTTCACTTGGAGGTAAACCACTGAACAACTACTGAGAGAA 466
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QY 467 GATGTTCAAGCTCTCTCGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGGA 526
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QY 527 GCGCCCTTAAGCTCGGATGGTGGGCTTTTGTGAGTGGCTGATGACAGGAGGAGGATGA 586
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QY 587 GGATGAGGAGGAGTATGATGAAGTGTCTCAGTGAAGTGAAGTGAAGGAGGAGGAGGATGA 646
DB 411 GGATGAGGAGGAGTATGATGAAGTGTCTCAGTGAAGTGAAGTGAAGGAGGAGGAGGATGA 352
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DB 111 CCCCTCCAATCTGCCCTGAA 88

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Job time : 1337.73 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :					GenEmbl :				
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6:	gb_pat.*	7:	gb_ph.*	8:	gb_pl.*	9:	gb_pr.*	10:	gb_ro.*
11:	gb_sts.*	12:	gb_sy.*	13:	gb_un.*	14:	gb_vt.*	15:	em_ba.*
16:	em_fun.*	17:	em_hum.*	18:	em_in.*	19:	em_mu.*	20:	em_om.*
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26:	em_ro.*	27:	em_sts.*	28:	em_un.*	29:	em_vt.*	30:	em_htg_hum.*
31:	em_htg_inv.*	32:	em_htg_other.*	33:	em_htg_mus.*	34:	em_htg_pln.*	35:	em_htg_rod.*
36:	em_htg_mam.*	37:	em_htg_vrt.*	38:	em_sy.*	39:	em_htgo_hum.*	40:	em_htgo_mus.*
41:	em_htgo_other.*								

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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c	3193.4	55.2	70449	9	AC105250	AC105250 Homo sapi
4	917.6	15.9	1136	9	BC007200	BC007200 Homo sapi
5	867.8	15.0	1052	6	AR009985	AR009985 Sequence
6	867.8	15.0	1052	6	I91514	I91514 Sequence 1
7	867.8	15.0	1052	6	I96074	I96074 Sequence 1
8	867.8	15.0	1052	9	HSU73477	HSU73477 Human acidi
c	794.8	13.7	162482	9	AC022740	AC022740 Homo sapi
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c	793.2	13.7	149015	9	AC107992	AC107992 Homo sapi
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14	764.4	13.2	925	9	AF025684	AF025684 Homo sapi
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19	649.6	11.2	980	6	I91515	I91515 Sequence 3
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22	640.4	11.1	750	9	HSU60823	U60823 Human poten
23	581	10.0	1656	9	AY007110	AY007110 Homo sapi
24	573.4	9.9	863	10	AF022957	AF022957 Mus muscu
25	569	9.8	771	9	BC000608	BC000608 Homo sapi
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43	272.8	4.7	1225	10	AB025581	AB025581 Rattus no
44	264.6	4.6	1397	10	BC003489	BC003489 Mus muscu
45	264.6	4.6	1408	10	BC005628	BC005628 Mus muscu

ALIGNMENTS

RESULT 1	AF008216	AF008216	5785 bp	DNA	linear	PRI 05-FEB-1999
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DEFINITION	AF008216	complete cds.				
ACCESSION	AF008216					
VERSION	AF008216.1	GI:2738512				
KEYWORDS						
SOURCE		Homo sapiens.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE		1 (bases 1 to 5785)				
		Kadkol,S.S., Brody,J.R., Pevsner,J., Bai,J. and Pasternack,G.R.				
		Modulation of oncogenic potential by alternative gene use in human				

Pred. No. is the number of results predicted by chance to have a

JOURNAL
REFERENCE
AUTHORS
TITLE
The Structure of a Gene Encoding pp32r1, a New Member of the pp32 Family
Unpublished
JOURNAL
REFERENCE
AUTHORS
TITLE
Submitted (13-JUN-1997) Pathology, Johns Hopkins University School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA
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BASE COUNT 1755 a 1087 c 1162 g 1781 t
ORIGIN
Query Match 100.0%; Score 5785; DB 9; Length 5785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AC079240/c
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ACCESSION   AC079240
VERSION     AC079240.6  GI:15431275
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 202847)
    Sultston,J.E. and Waterston,R.
    Toward a complete human genome sequence
    Genome Res. 8 (11), 1097-1108 (1998)
    99063792
    9847074
  2 (bases 1 to 202847)
    Tomlinson,C., Kozlowski,A., Phillips,A., Dixon,R. and Spalding,L.
    The sequence of Homo sapiens BAC clone RP11-808H17
    Unpublished (2001)
  3 (bases 1 to 202847)
    Waterston,R.H.
    Direct Submission
    Submitted (24-AUG-2000) Genome Sequencing Center, Washington
    University School of Medicine, 4444 Forest Park Parkway, St. Louis,
    MO 63108, USA
  4 (bases 1 to 202847)
    Waterston,R.H.
    Direct Submission
    Submitted (05-SEP-2001) Genome Sequencing Center, Washington
    University School of Medicine, 4444 Forest Park Parkway, St. Louis,
    MO 63108, USA
  5 (bases 1 to 202847)
    Waterston,R.
    Direct Submission
    Submitted (09-JAN-2002) Department of Genetics, Washington
    University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
    On Sep 5, 2001 this sequence version replaced gi:15145274.
    ----- Genome Center
    Center: Washington University Genome Sequencing Center
    Center code: WUGSC
    Web site: http://genome.wustl.edu/gsc
    Contact: sapiens@wustl.wustl.edu
    ----- Summary Statistics
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    Center project name: H_NH0808H17
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NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-39C10; the clone sequenced
to the right is RP11-277J14. Actual start of this clone is at base
position 1 of RP11-808H17; actual end is at base position 202847 of
RP11-808H17.

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Matches 4586; Conservative 0; Mismatches 4; Indels 32; Gaps 2;

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RESULT 3
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DEFINITION Homo sapiens BAC clone RP11-39C10 from 4, complete sequence.
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VERSION AC105250.3 GI:19310326
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 70449)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074
REFERENCE 2 (bases 1 to 70449)
Desai, A., Creason, K. and Kozlowski, A.
The sequence of Homo sapiens BAC clone RP11-39C10
Unpublished (2001)
REFERENCE 3 (bases 1 to 70449)
Waterston, R.H.
Direct Submission
Submitted (26-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 70449)
Waterston, R.
Direct Submission
Submitted (09-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 9, 2002 this sequence version replaced gi:18376931.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics
Center project name: H_NH0039C10
Drafting Center: WIBR
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E.,

Tateno, M., Catanesse, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org> VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-350H22, 2000 bp overlap; the clone sequenced to the right is RP11-808H17, 2000 bp overlap. Actual start of this clone is at base position 97207 of RP11-350H22; actual end is at base position 22714 of RP11-808H17.

The sequence of AC011026 has been incorporated into AC105250.

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Db 128 CGAGAGATGGAGTGGCAGACGGATTATTTAGAGCTGCGGAACGAGCGCCCTCTGAT 187
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RESULT 5
LOCUS AR009985
DEFINITION Sequence 1 from patent US 5756676.
ACCESSION AR009985
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AR009985 linear DNA 1052 bp PAT 04-DEC-1998

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VERSION AR009985.1 GI:3968790
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Mammalian protein associated with uncontrolled cell division
JOURNAL Patent: US 5756676-A 1 26-MAY-1998;
FEATURES
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        location/Qualifiers
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BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN
Query Match 15.0%; Score 867.8; DB 6; Length 1052;
Best Local Similarity 91.88; Pred. No. 1.2e-143;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;
Qy 4357 GAGTCTTCAAAGTCTCTAAACGTCGCGCCGTGGGTTCGAGGTTTATGTGATTCGCGC 4416
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Qy 4654 CTTGAACCTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCA 4704
Db 301 CTTGAACCTAAGCGATAACAGAGTCTCAGGGGCGCTAGAGTATTGGCAGAAAAAGTGTCCG 360
Qy 4705 AACCTCAGCATCTATATTAAAGTGGCAACAAAATTAAGACCTCAGCACCAATAGAGCCA 4764
Db 361 AACCTCAGCATCTAAATTTAAGTGGCAACAAAATTAAGACCTCAGCACCAATAGAGCCA 420
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QY 5245 ATCCCT-----CCGCCCTCCAATCCCTGCCCTGAAACTTACTTTTTCTGATTTAA 5298
Db 901 ATCCCTCTCCGCCCTCTAATCCTGCCCTGAAACTTACTTTTTCTGATTTAA 960
QY 5299 CATTGCTGTGGGAATGAGACGGGAAGTGTACTGGGGTGTGGAGGAGGAGGCGAG 5358
Db 961 CATTGCTGTGGGAATGAGACGGGAAGTGTACTGGGGTGTGGAGGAGGAGGCGAG 5358
QY 5359 GAGCGGTGGACTAAATACCTATTTTACTGCC 5391
Db 1020 GTGGGGTGGATTAATATCTATTTTACTGCC 1052

RESULT 6
191514
LOCUS 191514 1052 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5726018.
ACCESSION 191514
VERSION 191514.1 GI:3935984
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Nucleic acid based assays to detect a novel mammalian protein associated with uncontrolled cell division
JOURNAL Patent: US 5726018-A 1 10-MAR-1998;
FEATURES Location/Qualifiers
 source 1..1052
 BASE COUNT 326 a 196 c 316 g 214 t
 ORIGIN
 Query Match 15.0%; Score 867.8; DB 6; Length 1052;
 Best Local Similarity 91.8%; Pred. No. 1.2e-143;
 Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAAGTCTTAAACGTCGCGCGTTCGAGGTTTATTTGATTGATTCGGC 4416
Db 1 GAATTCCTCAAGTCTTAAACGTCGCGCGTTCGAGGTTTATTTGATTGATTCGGC 60
QY 4417 TGGCAGCAGAGCCCTCTCAGACAGAGAGCGCGAGAGATGGGACAGCGGATTCAT 4476
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QY 4477 TCAGAGCTGGGACAGGGGCCCTCTGATGTGAAGAACTTCCCTGGACACAGTCGG 4536
Db 121 TTAGAGTGGGAAACAGGAGCGCCCTCTGATGTGAAGAACTTCTCTGGACACAGTCGG 180
QY 4537 TCGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTCAAGAACTTGGAAATCTTAAGT 4596
Db 181 TCGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTCAAGAACTTGGAAATCTTAAGT 240
QY 4597 AAATCAACGAGGCGCCCTACCTCAATCTCAGACTTACCAAAGTTA---AAGTTGAGAAAG 4653
Db 241 ACAATCAACGTAGGCCCTCAGCTCAATCGCAAACTTACCAAAGTTAACAACCTTAAGAAG 300
QY 4654 CTTCGAACCTA-----AGAGTCTCAGGGGCTCGAAGTATTTGCGAGAAAAGTGTCCA 4704
Db 301 CTTCGAACCTAAGCGATACAGAGTCTCAGGGGCGCTAGAAGTATTTGCGAGAAAAGTGTCCG 360
QY 4705 AACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGACCTCAGACCAATAGAGCCA 4764
Db 361 AACCTCAGCATCTAATTTAAGTGGCAACAAATTAAGACCTCAGACCAATAGAGCCA 420
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QY 4825 AAGCACTACGGAGAAAACGTGTTCAAGTCTCTCCTGCAACTCACATATCTCGACAGCTGT 4884
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RESULT 7
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DEFINITION Sequence 1 from patent US 5734022.
ACCESSION 196074
VERSION 196074.1 GI:3940544
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Antibodies to a novel mammalian protein associated with uncontrolled cell division
JOURNAL Patent: US 5734022-A 1 31-MAR-1998;
FEATURES Location/Qualifiers
 source 1..1052
 BASE COUNT 326 a 196 c 316 g 214 t
 ORIGIN
 Query Match 15.0%; Score 867.8; DB 6; Length 1052;
 Best Local Similarity 91.8%; Pred. No. 1.2e-143;
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QY 4357 GAGTCTTCAAAGTCTTAAACGTCGCGCGTTCGAGGTTTATTTGATTGATTCGGC 4416
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QY	4945	GACGAGGAGGAGGTGAGCATGAGGAGGATGATGAAGATGCTCAGGTAGTGGAGAT	5004
Db	601	GATGAGGAGGAGTGAAGATGAGGAGGATGATGAAGATGCTCAGGTAGTGGAGAT	660
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QY	5065	GAGGATCAAGAAGGTTATAACGATGGAGAGGTAGATGCAGGAGGAGGAGGAGGAGGAGGAGG	5124
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QY	5125	GGTGAAGAAGAAAGGGGTGAGAAGCGAAGAAATGAGAAGCTCAAGATGAGGGAGAGAAGATGAT	5184
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DEFINITION		Homo sapiens chromosome 15, clone RP11-617D22, complete sequence.	
ACCESSION		AC022740	
VERSION		AC022740.4	GI:13786480
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SOURCE		Homo sapiens.	
ORGANISM		Homo sapiens	
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REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		Birren,B., Linton,L., Nusbaum,C. and Lander,E.	
JOURNAL		Homo sapiens chromosome 15, clone Rpl1-617D22	
REFERENCE		Unpublished	
AUTHORS		2 (bases 1 to 162482)	
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AUTHORS		Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,	
		Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,	
		Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,	
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Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K. T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shlm, C., Shoshkhari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, B., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, A., Thomas N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wouden, S., Worley, K., Wu, C., Wu, Y., Wu, F., Zhou, J., Zorilla, S., Kucherlapati, R., Weinstein, G., and Gibbs, R.

TITLE
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COMMENT

flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://9c.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

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	/rpt_family="(CAA)n"		
	1759..2636		
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	2662..3133		
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	3133..3390		
	/rpt_family="L1M4"		
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	6432..6642		
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Best Local Similarity 87.4%; Pred. No. 1.6e-130;			
Matches 935; Conservative 0; Mismatches 111; Indels 24; Gaps 5;			
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QY	4684	GTATTGGCAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAATTTAA	4743
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RESULT 11

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DEFINITION Homo sapiens chromosome 15, clone RP11-150L8, complete sequence.
ACCESSION AC107992
VERSION AC107992.3 GI:19683511
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149015)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-150L8
Unpublished
2 (bases 1 to 149015)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Farro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Linton,L., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149015)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Farro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
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Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
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Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
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Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
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Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
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Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
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Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149015)

TITLE

JOURNAL

REFERENCE

AUTHORS

Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 149015)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Linton,L., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
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Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H.,
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Direct Submission
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Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 149015)

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project information
Center project name: L24554
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VERSION AC16297.4 GI:15022083
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186886)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Bozulavkiy,L., Boukhgaltier,B.,
Brown,A., Castie,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Doneilan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 26, 2001 this sequence version replaced gi:7139678.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4280
Center clone name: 82-L14
----- Summary Statistics
Sequencing vector: M13; M77815; 96% of reads
Sequencing vector: Plasmid; n/a; 4% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 179979 bases at least Q40
Consensus quality: 183319 bases at least Q30
Consensus quality: 184541 bases at least Q20
Insert size: 185000; agarose-fp
Quality coverage: 185486; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; agarose-fp
Quality coverage: 5.3 in Q20 bas.
* NOTE: This is a 'working draft' sequence. It currently

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* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 28840: contig of 28840 bp in length
* 28841 28940: gap of 100 bp
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* 30180 30279: gap of 100 bp
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* 37563 37662: gap of 100 bp
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* 41177 41276: gap of 100 bp
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* 76173 76272: gap of 100 bp
* 76273 83570: contig of 7298 bp in length
* 83571 83670: gap of 100 bp
* 83671 92374: contig of 8704 bp in length
* 92375 92474: gap of 100 bp
* 92475 100960: contig of 8486 bp in length
* 100961 101060: gap of 100 bp
* 101061 110544: contig of 9484 bp in length
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* 124450 124549: gap of 100 bp
* 124550 142962: contig of 18413 bp in length
* 142963 143062: gap of 100 bp
* 143063 164019: contig of 20957 bp in length
* 164020 164119: gap of 100 bp
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RESULT 14
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DEFINITION Homo sapiens cerebellar leucine rich acidic nuclear protein (LANP)
ACCESSION AF025684
VERSION AF025684.1 GI:2589220
KEYWORDS mRNA, complete cds.
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 925)
Matilla,A., Koshy,B.T., Cummings,C.J., Isobe,T., Orr,H.T. and
Zoghbi,H.Y.

TITLE	The cerebellar leucine-rich acidic nuclear protein interacts with ataxin-1
JOURNAL	Nature 389 (6654), 974-978 (1997)
MEDLINE	98013170
PUBMED	9353121
REFERENCE	2 (bases 1 to 925)
AUTHORS	Matilla,A. and Zoghbi,H.Y.
TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-1997) Molecular and Human Genetics, and Pediatrics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Db	923	TCC	925
RESULT 15			
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DEFINITION	Rattus norvegicus		
ACCESSION	D32209		
VERSION	D32209.1 GI:511663		
KEYWORDS	leucine-rich acidic nuclear protein; leucine-rich repeat; nuclear factor.		
SOURCE	Rattus norvegicus (strain Wistar) (library: library of M.Taoka) postnatal days 7 brain cDNA to mRNA, clone PRN-8.		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
	1 (bases 1 to 1017)		
AUTHORS	Matsuoka,K., Taoka,M., Satozawa,N., Nakayama,H., Ichimura,T., Takahashi,N., Yamakuni,T., Song,S.Y. and Isobe,T.		
	A nuclear factor containing the leucine-rich repeats expressed in murine cerebellar neurons		
TITLE	Proc. Natl. Acad. Sci. U.S.A. 91 (21), 9670-9674 (1994)		
JOURNAL	95024022		
MEDLINE	2 (bases 1 to 1017)		
REFERENCE	Matsuoka,K.		
AUTHORS	Direct Submission		
TITLE	Submitted (18-JUL-1994) Kunie Matsuoka, Mitsubishi Kasei Institute of Life Science, 11 Minami-Oya, Machida, Tokyo 194, Japan		
JOURNAL	(Tel:0427-24-6288, Fax:0427-24-6316)		
COMMENT	Submitted (18-Jul-1994) to DDBJ by:		
	Kunie Matsuoka		
FEATURES	Mitsubishi Kasei Institute of Life Science		
	11 Minami-Oya, Machida		
source	Tokyo 194		
	Japan		
source	Phone: 0427-24-6288		
	Fax: 0427-24-1252.		
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QY	5068	GATGAAGAAGGTTATAACGATGGAGAGGTAGATGGCGGAGGAAGATGAAGAAGAGCTTGGT	5127
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Search completed: December 8, 2002, 18:46:26
Job time : 12839 secs

phosphoprotein 32 (pp32) related genomic sequences

XX Claim 1; Fig 2; 65pp; English.

XX The present sequence represents the genomic sequence of phosphoprotein

CC 32 (pp32) variant pp32r1, which is isolated from human placenta. The

CC pp32r1 and pp32r2 sequences are associated with cancer in prostate, especially prostatic adenocarcinomas. Normal pp32 exerts antineoplastic

CC activity through suppression of transformation. Cancer-associated pp32

CC variants augment, rather than inhibit, transformation. Determining the

CC presence of a gene encoding residues 146-163 of pp32r1 or pp32r2 in a

CC sample is useful for a diagnostic method for predicting malignant

CC potential of neuroendocrine, neural, mesenchymal, lymphoid, epithelial

CC or germ cell-derived tumours.

XX

SQ Sequence 5785 BP; 1755 A; 1087 C; 1162 G; 1781 T; 0 other;

Query Match 100.0%; Score 5785; DB 20; Length 5785;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTTTTCCTTATGTAAGTCTCTAATCAACATAGCATATGTTTTCATGTTTTCCTCCCT 120

DB 61 CTTTTCCTTATGTAAGTCTCTAATCAACATAGCATATGTTTTCATGTTTTCCTCCCT 120

QY 121 ATCAGTTGCAAGTTCACAGAGCTGATATATTTTCATTTTCATTCGGCTACTATAGCCCTA 180

DB 121 ATCAGTTGCAAGTTCACAGAGCTGATATATTTTCATTTTCATTCGGCTACTATAGCCCTA 180

QY 181 GAGCTGCACATAGTTTTCGGCTGTAAGTGCATATAATATTTTGTAAATGAGTAGAAA 240

DB 181 GAGCTGCACATAGTTTTCGGCTGTAAGTGCATATAATATTTTGTAAATGAGTAGAAA 240

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QY 361 ACTAAGGAATTTGGACATTAATCAAGCTAGCTTTCTATACAAATAACTGAATTC 420

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QY 841 CCCAACTACTAGGAGGCTGAGCAGAGAAATCGCTTGAACCTGGGAGCGAGGTGCA 900

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QY 4321 TAAATATTTGGGCTCGAAGACCGAGCGAGCTGGTTGAGTCTTCAAAGTCTCAAACGTG 4380
|||||
Db 4321 TAAATATTTGGGCTCGAAGACCGAGCGAGCTGGTTGAGTCTTCAAAGTCTCAAACGTG 4380
QY 4381 CGGCCGTGGGTCGAGGTTTATTGATTGAATTCGAATTCGGCTGGCACGAGAGCTCTCGCAGACAG 4440
|||||
Db 4381 CGGCCGTGGGTCGAGGTTTATTGATTGAATTCGAATTCGGCTGGCACGAGAGCTCTCGCAGACAG 4440
QY 4441 AGAGCCGAGAGATGGAGATGGGCAGACGGATTCAATCAGAGCTGCGGAACAGGGCGCCC 4500
|||||
Db 4441 AGAGCCGAGAGATGGAGATGGGCAGACGGATTCAATCAGAGCTGCGGAACAGGGCGCCC 4500
QY 4501 TCTGATGTGAAGAATTTGCCCTGGACACACAGTCGGTTCGAATGAAGCGAACTCGAAGCC 4560
|||||
Db 4501 TCTGATGTGAAGAATTTGCCCTGGACACACAGTCGGTTCGAATGAAGCGAACTCGAAGCC 4560
QY 4561 CTCACAGATGAATTTGAAGAATCGAAATCTTAAAGTAAATCAACGGAGGCTCACCTCA 4620
|||||
Db 4561 CTCACAGATGAATTTGAAGAATCGAAATCTTAAAGTAAATCAACGGAGGCTCACCTCA 4620
QY 4621 ATCTCAGACTTACCAAAGTTAAAGTTGAGAAGCTTGAACCTTAAGAGTCTCAGGGGGCGTG 4680
|||||
Db 4621 ATCTCAGACTTACCAAAGTTAAAGTTGAGAAGCTTGAACCTTAAGAGTCTCAGGGGGCGTG 4680
QY 4681 GAAGTATTTGGCAGAAAGTGTCCAAACCTCACGCATCTATATTAAGTGGCAACAAATTT 4740
|||||
Db 4681 GAAGTATTTGGCAGAAAGTGTCCAAACCTCACGCATCTATATTAAGTGGCAACAAATTT 4740
QY 4741 AAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGAAAAACCTCAAGAGCTTAGACCTT 4800
|||||
Db 4741 AAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGAAAAACCTCAAGAGCTTAGACCTT 4800
QY 4801 TTCAATTCGGAGGTAAACCAACCTGAACGACTACGAGAGAAAACGTGTCAAGCTTCTCCTG 4860
|||||
Db 4801 TTCAATTCGGAGGTAAACCAACCTGAACGACTACGAGAGAAAACGTGTCAAGCTTCTCCTG 4860
QY 4861 CAACCTCACATATCTCGACAGCTGTACTTGGGACCACAGGAGGCGCCCTTACTCAGATATT 4920
|||||
Db 4861 CAACCTCACATATCTCGACAGCTGTACTTGGGACCACAGGAGGCGCCCTTACTCAGATATT 4920
QY 4921 GAGGACCACTCGAGGGCTTGATCAGCAGGAGGAGGCTGAGCATGAGGAGGAGTATGAT 4980
|||||
Db 4921 GAGGACCACTCGAGGGCTTGATCAGCAGGAGGAGGCTGAGCATGAGGAGGAGTATGAT 4980
QY 4981 GAAGATGCTCAGGTAGTGGAGATGAGGAGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
|||||
Db 4981 GAAGATGCTCAGGTAGTGGAGATGAGGAGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
QY 5041 GAGGAGCTCAGTGGAGGCGACCGACGAGCATGAAGAGCTTAAACGATGGAGAGGTAGAT 5100
|||||
Db 5041 GAGGAGCTCAGTGGAGGCGACCGACGAGCATGAAGAGCTTAAACGATGGAGAGGTAGAT 5100
QY 5101 GCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAAGACGAAAAATGAGAA 5160
|||||
Db 5101 GCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAAGACGAAAAATGAGAA 5160
QY 5161 CCTGAAGATGAGGGAGAGATGATGACTAAGTAGAATAACCTATTTTGAATAATTCCTAT 5220

Db 5161 CCTGAAGATGAGGAGAGAAGATGATGACTAAGTAGAATAACCTATTTTGAATAATTCCTAT 5220
QY 5221 TGTGATTTGACTCTTTTACCCTATATCCCTCCCTCCCAATCCTGCCCCCTGAAACTTT 5280
Db 5221 TGTGATTTGACTCTTTTACCCTATATCCCTCCCTCCCAATCCTGCCCCCTGAAACTTT 5280
QY 5281 ACTTTTTTCTGATTTGTAACATTTCTGTGGGAATGAGACGGGAAAAGTGTACTGGGGTTG 5340
Db 5281 ACTTTTTTCTGATTTGTAACATTTCTGTGGGAATGAGACGGGAAAAGTGTACTGGGGTTG 5340
QY 5341 TGGAGGAGGAGGGCAGGAGCGGTGGACTAAAAATACATATTTTACTGCCAAATAAAAT 5400
Db 5341 TGGAGGAGGAGGGCAGGAGCGGTGGACTAAAAATACATATTTTACTGCCAAATAAAAT 5400
QY 5401 AATATTTGTAATAATTAACCTGGGATACACTAGCTTTGTAGAATGATTACTATTAATTCT 5460
Db 5401 AATATTTGTAATAATTAACCTGGGATACACTAGCTTTGTAGAATGATTACTATTAATTCT 5460
QY 5461 CTCTCTCTTTTATTTTACACATTTCTTTTAAAGTATAGTCCCTTTAGTCCAAG 5520
Db 5461 CTCTCTCTTTTATTTTACACATTTCTTTTAAAGTATAGTCCCTTTAGTCCAAG 5520
QY 5521 GAAAGGCACCTACAATCCACTTATTAATGCTTGTCTACTGTGTTCAAGTAAAAATAGCTCC 5580
Db 5521 GAAAGGCACCTACAATCCACTTATTAATGCTTGTCTACTGTGTTCAAGTAAAAATAGCTCC 5580
QY 5581 AGGATTTAACAAAAGAGGAAAGAAAATTTTACAATGAAATGTTGCTAAAAATTTAAA 5640
Db 5581 AGGATTTAACAAAAGAGGAAAGAAAATTTTACAATGAAATGTTGCTAAAAATTTAAA 5640
QY 5641 ACAATTTACAGTAAATGTTTAAAGCAAAATTTCTATTTTAAAAATTTATTAATAAGGA 5700
Db 5641 ACAATTTACAGTAAATGTTTAAAGCAAAATTTCTATTTTAAAAATTTATTAATAAGGA 5700
QY 5701 AATAATTTGCTAAAGCAAAATTTTGGAAAAATAAATGACACTTTTACTTGATTTATTT 5760
Db 5701 AATAATTTGCTAAAGCAAAATTTTGGAAAAATAAATGACACTTTTACTTGATTTATTT 5760
QY 5761 TATTAACAATGATTTATAAGCTT 5785
Db 5761 TATTAACAATGATTTATAAGCTT 5785

RESULT 2
AAA88236
ID AAA88236 standard; DNA; 5785 BP.
XX
AC AAA88236;
XX
DT 15-DEC-2000 (first entry)
XX
DE Human placenta variant pp32rl genomic DNA sequence.
XX
KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200045852-A1.
XX
PD 10-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US02656.
XX
PR 03-FEB-1999; 99US-0118667.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Pasternack GR, Bai J;
XX
DR WPI; 2000-514896/46.

XX Treatment of cancer comprising restoration of pp32 function in
PT malignant cells -
XX

Example 3; Fig 2; 90pp; English.

CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human placenta variant pp32r1 genomic DNA sequence from
CC an example of the present invention.

XX Sequence 5785 BP; 1755 A; 1087 C; 1162 G; 1781 T; 0 other;

Query Match		100.0%;	Score 5785;	DB 21;	Length 5785;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 5785;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AAGCTTTCCTGATCTCTAAATCAAGGTCAGCTCCCTAAGCTCTTGGCTCCGGTACTGAAA	60		
Db	1	AAGCTTTCCTGATCTCTAAATCAAGGTCAGCTCCCTAAGCTCTTGGCTCCGGTACTGAAA	60		
Qy	61	CTTTTCTTATGTAACCTCTATAACACATAGCATATGTTTCGATGTTTCTTCCCT	120		
Db	61	CTTTTCTTATGTAACCTCTATAACACATAGCATATGTTTCGATGTTTCTTCCCT	120		
Qy	121	ATCAGTTCCAGATTCACAGCAGCTGATATATTTTCATTTTCATTCGCTACTATAGCCCTA	180		
Db	121	ATCAGTTCCAGATTCACAGCAGCTGATATATTTTCATTTTCATTCGCTACTATAGCCCTA	180		
Qy	181	GAGCCTGACATAGTTTCGGCTGTGAATGCTCAATAATATTTGTTAAATGAGTAGAAA	240		
Db	181	GAGCCTGACATAGTTTCGGCTGTGAATGCTCAATAATATTTGTTAAATGAGTAGAAA	240		
Qy	241	CATAAGTATCTATTTTCATTCGAAGGAAAGATAATAGCTACATTTTCTTTTCTTGCC	300		
Db	241	CATAAGTATCTATTTTCATTCGAAGGAAAGATAATAGCTACATTTTCTTTTCTTGCC	300		
Qy	301	TTAATATTTGAGGAAATTTGCTTATATGTCATAATAAAGTTAAAGCCTTATACATAT	360		
Db	301	TTAATATTTGAGGAAATTTGCTTATATGTCATAATAAAGTTAAAGCCTTATACATAT	360		
Qy	361	ACTAAGGAATTTGGACATTAATCAAGCTAGCCTTCTTATAACAAATFACGAATTC	420		
Db	361	ACTAAGGAATTTGGACATTAATCAAGCTAGCCTTCTTATAACAAATFACGAATTC	420		
Qy	421	TGTCCTAAATTTGTTCTTCCCTATTTCTCCCATTCAGATGACACCAATCCCTCTAG	480		
Db	421	TGTCCTAAATTTGTTCTTCCCTATTTCTCCCATTCAGATGACACCAATCCCTCTAG	480		
Qy	481	CTGCTCAAAACCAAGTACCGTATGTTATTTCTTAATFATCTCTTTACCTTGCTTCATAT	540		
Db	481	CTGCTCAAAACCAAGTACCGTATGTTATTTCTTAATFATCTCTTTACCTTGCTTCATAT	540		
Qy	541	GCAATTTGTTAACAAGTCACTTCAAGTCTGATCCCAACTCTTGCTCTACTTAAATTCAT	600		
Db	541	GCAATTTGTTAACAAGTCACTTCAAGTCTGATCCCAACTCTTGCTCTACTTAAATTCAT	600		
Qy	601	ACATGCTGTGACTACTGCTACATAGCTCCCAACTCTTGCTCTACTTAAATTCAT	660		
Db	601	ACATGCTGTGACTACTGCTACATAGCTCCCAACTCTTGCTCTACTTAAATTCAT	660		
Qy	661	GTAATAATCAGTCTTGGCGGGCAGCGGTGGCTCACACCTATAATCCAGCAGCTTTGGGA	720		
Db	661	GTAATAATCAGTCTTGGCGGGCAGCGGTGGCTCACACCTATAATCCAGCAGCTTTGGGA	720		

Qy	721	GTCCAGGCGGGGTACAGAGTCAAGAGATGAGAGCCATCATGGCCAAACATGGTGA	780
Db	721	GTCCAGGCGGGGTACAGAGTCAAGAGATGAGAGCCATCATGGCCAAACATGGTGA	780
Qy	781	ACCTCTCTCTACTATAAATACAAAAAATATCTGGGTGTGGTGGCAGATCCCTGTAA	840
Db	781	ACCTCTCTCTACTATAAATACAAAAAATATCTGGGTGTGGTGGCAGATCCCTGTAA	840
Qy	841	CCCACTACTAGGAGGCTGAGGAGGAATCGCTTGAACCTGGGAGGCGGAGGTGCA	900
Db	841	CCCACTACTAGGAGGCTGAGGAGGAATCGCTTGAACCTGGGAGGCGGAGGTGCA	900
Qy	901	GTGAGCGAGATCGCACCATTGCACCTCCAGCTGGCAACAGAGCAGAGATCCATCCAAA	960
Db	901	GTGAGCGAGATCGCACCATTGCACCTCCAGCTGGCAACAGAGCAGAGATCCATCCAAA	960
Qy	961	ACAAAAACAAAAACCAACCATGTCTGTAAAAACATGTCTGTAAAAACATGTCTGTAA	1020
Db	961	ACAAAAACAAAAACCAACCATGTCTGTAAAAACATGTCTGTAAAAACATGTCTGTAA	1020
Qy	1021	AGTCTTACATGCTTTTTCATATGCTAAGATAAAAAACCAAAATGCAATTTCTTGGTTCT	1080
Db	1021	AGTCTTACATGCTTTTTCATATGCTAAGATAAAAAACCAAAATGCAATTTCTTGGTTCT	1080
Qy	1081	AAGCCCAAGAAAAATAGAGTTGCTTTTCAGCAACCTTGTCTTCCGCCATGCTTTCCCT	1140
Db	1081	AAGCCCAAGAAAAATAGAGTTGCTTTTCAGCAACCTTGTCTTCCGCCATGCTTTCCCT	1140
Qy	1141	AGTCTACTCTTTTAGGCAAGTCGACCTGATTTCTTCTGTGTAGTCTGTCTTGGCTCTCA	1200
Db	1141	AGTCTACTCTTTTAGGCAAGTCGACCTGATTTCTTCTGTGTAGTCTGTCTTGGCTCTCA	1200
Qy	1201	TGCTCTGGCTCTTCTTCTGTGTAGTCTGTGTTCACCTCGGCTGTGGCTCTTCA	1260
Db	1201	TGCTCTGGCTCTTCTTCTGTGTAGTCTGTGTTCACCTCGGCTGTGGCTCTTCA	1260
Qy	1261	TTCTGGCTGGAATGCTCTCCACCTCCAGATCTTACTAGATCTTACTAGTCAATCACCT	1320
Db	1261	TTCTGGCTGGAATGCTCTCCACCTCCAGATCTTACTAGATCTTACTAGTCAATCACCT	1320
Qy	1321	CGCAGGAAGATCTTCAACCATTCACCTGCATACACCTATGGCTGCTCCCTAGAGAACAT	1380
Db	1321	CGCAGGAAGATCTTCAACCATTCACCTGCATACACCTATGGCTGCTCCCTAGAGAACAT	1380
Qy	1381	CATTCTGTTTCTTCTACCTTCTAGCAGTCTACTGCTTCTTCTGAAATFATCTACTTTGAT	1440
Db	1381	CATTCTGTTTCTTCTACCTTCTAGCAGTCTACTGCTTCTTCTGAAATFATCTACTTTGAT	1440
Qy	1441	TTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC	1500
Db	1441	TTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC	1500
Qy	1501	TTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC	1560
Db	1501	TTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC	1560
Qy	1561	AATCGTTAAATGATAAATTTTGAAGAAGATAATTTGGGATCCATTTAGTTGCA	1620
Db	1561	AATCGTTAAATGATAAATTTTGAAGAAGATAATTTGGGATCCATTTAGTTGCA	1620
Qy	1621	ACATTTCTATCTGTCTGTAGACAGAGGCGCATGTGTAAGGACAAAGACATATTTATAG	1680
Db	1621	ACATTTCTATCTGTGTAGACAGAGGCGCATGTGTAAGGACAAAGACATATTTATAG	1680
Qy	1681	ACTGTACCTCGAAAAATAAATAAATTTGAACCTTGAACAGCTTATACAGAGTATGTG	1740
Db	1681	ACTGTACCTCGAAAAATAAATAAATTTGAACCTTGAACAGCTTATACAGAGTATGTG	1740
Qy	1741	AGGTACAGTTATATTTAGAAATGGTAAATCACCCTTCTTAAGCATTAATCTAGACACA	1800
Db	1741	AGGTACAGTTATATTTAGAAATGGTAAATCACCCTTCTTAAGCATTAATCTAGACACA	1800

QY	1801	TATTAGAGGTAGAGAGAGAAGTGCCTCTTAGATATTTGGTAATCATATATTAGACTGACGC	1860	Db	2881	AA	2940
Db	1801	TATTAGAGGTAGAGAGAGAAGTGCCTCTTAGATATTTGGTAATCATATATTAGACTGACGC	1860	QY	2941	AGTAAAGGTGTACAGAGCAAGCAATATTGTGAGAACTACACAGGCAAGCTTACTTTCAAG	3000
QY	1861	CATCCTTGATTTTTCTCTGGGAAACAGCTCAAAATGACTATTATTAATGTTTACAATGATA	1920	Db	2941	AGTAAAGGTGTACAGAGCAAGCAATATTGTGAGAACTACACAGGCAAGCTTACTTTCAAG	3000
Db	1861	CATCCTTGATTTTTCTCTGGGAAACAGCTCAAAATGACTATTATTAATGTTTACAATGATA	1920	QY	3001	GCAGTTTATGTAAGCTCAATTCATTTGCTCAGTGTCTTGTGCTATGTGTGGTGTATAGGAT	3060
QY	1921	TCNTGCATCTTGGCAGTAATAATATATATAGACACTAGGAATCCAAATTTGAAGATGAAC	1980	Db	3001	GCAGTTTATGTAAGCTCAATTCATTTGCTCAGTGTCTTGTGCTATGTGTGGTGTATAGGAT	3060
Db	1921	TCNTGCATCTTGGCAGTAATAATATATAGACACTAGGAATCCAAATTTGAAGATGAAC	1980	QY	3061	TTGGAACATATGATCAATCTGAGCACACATCAGTAAACTGAATAGGATTAATAAATCCA	3120
QY	1981	AAGTCTTTATAGAGGAGAGCCAAAATACACAATAAATAACACAAGGTGTAATACAGTA	2040	Db	3061	TTGGAACATATGATCAATCTGAGCACACATCAGTAAACTGAATAGGATTAATAAATCCA	3120
Db	1981	AAGTCTTTATAGAGGAGAGCCAAAATACACAATAAATAACACAAGGTGTAATACAGTA	2040	QY	3121	CAAGCATTTTACTAGTGGAACTCTGTGATATTTCTAGCTACTCTTGTCTGTATTTATTTGA	3180
QY	2041	ATACAAACATACATACCATGCAATAGAGTGCAGAGAGGTGCTCTCCGAATGCAGTC	2100	Db	3121	CAAGCATTTTACTAGTGGAACTCTGTGATATTTCTAGCTACTCTTGTCTGTATTTATTTGA	3180
Db	2041	ATACAAACATACATACCATGCAATAGAGTGCAGAGAGGTGCTCTCCGAATGCAGTC	2100	QY	3181	ATCTTTTGTCTCATATCCTATAGTAAGATTTTCAGGAAATATATTTTATTTGCTCAGAA	3240
QY	2101	ACCCAGAAAGTCCCTCTGTAGAAAGGATATCTTAAATGGTGTCTTAAAGGAAAAGTAACC	2160	Db	3181	ATCTTTTGTCTCATATCCTATAGTAAGATTTTCAGGAAATATATTTTATTTGCTCAGAA	3240
Db	2101	ACCCAGAAAGTCCCTCTGTAGAAAGGATATCTTAAATGGTGTCTTAAAGGAAAAGTAACC	2160	QY	3241	TTTAGCCCTTTAGTTTTTGTGAATCTATTGCTCATATTTCTTATAGTAAGAGTTTCAGGAA	3300
QY	2161	AAAGGCAACTAAAGATTGCAAGAGGTCCCGAGAAAGCAAAAGCAAGGTACATA	2220	Db	3241	TTTAGCCCTTTAGTTTTTGTGAATCTATTGCTCATATTTCTTATAGTAAGAGTTTCAGGAA	3300
Db	2161	AAAGGCAACTAAAGATTGCAAGAGGTCCCGAGAAAGCAAAAGCAAGGTACATA	2220	QY	3301	TGTATTTCTATTGCTGTGGAAATTTAGCCCTTCAGGTTTTTGAGCCCTCTTTTGTCTTAT	3360
QY	2221	GGCAGAAAAGTACGCTGCTCTGGGAACTTCCCAATAGTTTGGTGGAGCACACAGTTAG	2280	Db	3301	TGTATTTCTATTGCTGTGGAAATTTAGCCCTTCAGGTTTTTGAGCCCTCTTTTGTCTTAT	3360
Db	2221	GGCAGAAAAGTACGCTGCTCTGGGAACTTCCCAATAGTTTGGTGGAGCACACAGTTAG	2280	QY	3361	GGGACATAGTATGACAGCAAGATGAATGACTTCTATTCCTCAATTCACATGATGGGAAA	3420
QY	2281	AAGTACTGTGCCATGGAGCAAGACTGAAGACATATGCAGGTTCGAAGGCCACAGAGCCC	2340	Db	3361	GGGACATAGTATGACAGCAAGATGAATGACTTCTATTCCTCAATTCACATGATGGGAAA	3420
Db	2281	AAGTACTGTGCCATGGAGCAAGACTGAAGACATATGCAGGTTCGAAGGCCACAGAGCCC	2340	QY	3421	ATGAAGCAAAAATGTTTATTCACCTCAAGGCTCTGCCATGTTTCTCTGGTGGAAATACGGC	3480
QY	2341	CATATATGTCATGAATGATATTTGGAGCCACTGGGAGCTACTGAACTTTAAGCAGG	2400	Db	3421	ATGAAGCAAAAATGTTTATTCACCTCAAGGCTCTGCCATGTTTCTCTGGTGGAAATACGGC	3480
Db	2341	CATATATGTCATGAATGATATTTGGAGCCACTGGGAGCTACTGAACTTTAAGCAGG	2400	QY	3481	TCACACACAAATTTCCCTAAATGCCCTGTCTGTCTCAATAGACACATATTAATTT	3540
QY	2401	GAATAAAATTTGTATATCTACACCTTAGAAAATTTGATTTTTTCTCTCTTTATATCTTC	2460	Db	3481	TCACACACAAATTTCCCTAAATGCCCTGTCTGTCTCAATAGACACATATTAATTT	3540
Db	2401	GAATAAAATTTGTATATCTACACCTTAGAAAATTTGATTTTTTCTCTCTTTATATCTTC	2460	QY	3541	TATCTTCTCTCGAGTGTCTTCCACAAATCCCATAGCCCTGTGAAAAGATGTTTATAGGG	3600
QY	2461	TCCT	2520	Db	3541	TATCTTCTCTCGAGTGTCTTCCACAAATCCCATAGCCCTGTGAAAAGATGTTTATAGGG	3600
Db	2461	TCCT	2520	QY	3601	AAATATTTATTTTAAATATAGCATATTTTGTCAATGTGGGACATAGGACTAGTACCTGCTG	3660
QY	2521	GTGTGTGTGTGACAGAGTCCCTCTGTACCCAGGCTGGAGTGTAGTGGAGTATCTCC	2580	Db	3601	AAATATTTATTTTAAATATAGCATATTTTGTCAATGTGGGACATAGGACTAGTACCTGCTG	3660
Db	2521	GTGTGTGTGTGACAGAGTCCCTCTGTACCCAGGCTGGAGTGTAGTGGAGTATCTCC	2580	QY	3661	AAAACCATCTCATGATCCTTGTGTGAACAACTAATTCACACTAGAAAATACATTTTCTCTTG	3720
QY	2581	GCTTACTGCAGTCTCTGCTCTCAAGCGATTCCTTGCCTCAGCCCTCCGAGTGTAGTGGGA	2640	Db	3661	AAAACCATCTCATGATCCTTGTGTGAACAACTAATTCACACTAGAAAATACATTTTCTCTTG	3720
Db	2581	GCTTACTGCAGTCTCTGCTCTCAAGCGATTCCTTGCCTCAGCCCTCCGAGTGTAGTGGGA	2640	QY	3721	CTCATTTAAAACATATAATGTCTCAGAAAGTAAAAATTTATTCCTCTCTAAATAAACAATAC	3780
QY	2641	TTACAGCGGGCTCTACACAGCTGGCTAACTTTTGTATTTTGGTAACCAACCAAGGTTT	2700	Db	3721	CTCATTTAAAACATATAATGTCTCAGAAAGTAAAAATTTATTCCTCTCTAAATAAACAATAC	3780
Db	2641	TTACAGCGGGCTCTACACAGCTGGCTAACTTTTGTATTTTGGTAACCAACCAAGGTTT	2700	QY	3781	ATGCCACTCAAAATTTTATTCCTCTACCACTTGCCTGTATCTAAACCTAGTTAGATCTTTG	3840
QY	2701	TACCATTTTGGCCAGGCTGCTCTCAACTCCTGACCTCAGGTGATCTGCCCTGGCTTG	2760	Db	3781	ATGCCACTCAAAATTTTATTCCTCTACCACTTGCCTGTATCTAAACCTAGTTAGATCTTTG	3840
Db	2701	TACCATTTTGGCCAGGCTGCTCTCAACTCCTGACCTCAGGTGATCTGCCCTGGCTTG	2760	QY	3841	GTTTTAGGTATAATCTGACAGAACAGATACCAAGATCACATTTGTAGTCAAGAGTGG	3900
QY	2761	TTCCAAAGTGTGGATATACAGCGGTGAGCCACCCGCTGCTGTGTAGAGTTTGTATTTG	2820	Db	3841	GTTTTAGGTATAATCTGACAGAACAGATACCAAGATCACATTTGTAGTCAAGAGTGG	3900
Db	2761	TTCCAAAGTGTGGATATACAGCGGTGAGCCACCCGCTGCTGTGTAGAGTTTGTATTTG	2820	QY	3901	AAAATTCATTAATTCATGATGATACCAATAAAGATAGATTTAGCTTTTACAGGATGTTT	3960
QY	2821	ATGTCAGTGTGTAGATGAATTTTGGGAGCAAAACAAAGATAGATTTCAATGACAGTGA	2880	Db	3901	AAAATTCATTAATTCATGATGATACCAATAAAGATAGATTTAGCTTTTACAGGATGTTT	3960
Db	2821	ATGTCAGTGTGTAGATGAATTTTGGGAGCAAAACAAAGATAGATTTCAATGACAGTGA	2880	QY	3961	TTGGCATTTTATTTCTTTTCATTTTGGGGAGATCTCACCAGAAATATGCTTTTCATGTTCA	4020
QY	2881	AAAGTTTATTTATTAAGCTATATAAAGAAAATGTTGAAGGTTTGAATCCATTAGTGGC	2940				

Db 3961 TTGCGATTTTATCTTTTCATTTGAGGGGAGATCTCACAAAATATGCTCTTTCATGGTTCA 4020
QY 4021 TTGCTGTATTTAAATTTCTGTCATGCATATCTTCAGGTACTTTTAAACCTAGTCTATAGAT 4080
Db 4021 TTGCTGTATTTAAATTTCTGTCATGCATATCTTCAGGTACTTTTAAACCTAGTCTATAGAT 4080
QY 4081 TCAAGAGATATCCCGTGTCCAGTCTCTAAAGTAAAGAAAGAAATGGGTACTTGTGAAGGC 4140
Db 4081 TCAAGAGATATCCCGTGTCCAGTCTCTAAAGTAAAGAAAGAAATGGGTACTTGTGAAGGC 4140
QY 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTGCCCTTGTGTAATTCACAAATATCAACGTGA 4200
Db 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTGCCCTTGTGTAATTCACAAATATCAACGTGA 4200
QY 4201 GCATCAGATAAGATTTTCTTTAGTGCACACACACCTACCTCTTACTAGGAGATCCATAT 4260
Db 4201 GCATCAGATAAGATTTTCTTTAGTGCACACACACCTACCTCTTACTAGGAGATCCATAT 4260
QY 4261 ACTTGAATAATTTGTTCTGTTGACCCAGGTTACTTATCAGTCCCTTTATTAATAATTTTG 4320
Db 4261 ACTTGAATAATTTGTTCTGTTGACCCAGGTTACTTATCAGTCCCTTTATTAATAATTTTG 4320
QY 4321 TAAATATTTGGGCTCGAGAACCGGAGCGAGCTGGTTGAGTCTTCAAAAGTCTTAAACGTG 4380
Db 4321 TAAATATTTGGGCTCGAGAACCGGAGCGAGCTGGTTGAGTCTTCAAAAGTCTTAAACGTG 4380
QY 4381 CGGCGTGGGTTTCGAGGTTTATTCATTTGAATTCGGCTGGCAGAGAGCCCTTCGACAGAC 4440
Db 4381 CGGCGTGGGTTTCGAGGTTTATTCATTTGAATTCGGCTGGCAGAGAGCCCTTCGACAGAC 4440
QY 4441 AGAGCGGAGAGATGGAGATGGGAGCGGATTCATTTCAGAGTTCGCGAAGACAGGGCGCCC 4500
Db 4441 AGAGCGGAGAGATGGAGATGGGAGCGGATTCATTTCAGAGTTCGCGAAGACAGGGCGCCC 4500
QY 4501 TCTGATGTGAAGAACTTGCCTCGACACAGCTCGGTGCGAATGAAGCCAACTCGAAGCC 4560
Db 4501 TCTGATGTGAAGAACTTGCCTCGACACAGCTCGGTGCGAATGAAGCCAACTCGAAGCC 4560
QY 4561 CTCACAGATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCA 4620
Db 4561 CTCACAGATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCA 4620
QY 4621 ATCTCAGACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGCGCTG 4680
Db 4621 ATCTCAGACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGCGCTG 4680
QY 4681 GAAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGCGCAACAAAT 4740
Db 4681 GAAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGCGCAACAAAT 4740
QY 4741 AAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAGAGAGCTTAGACCTT 4800
Db 4741 AAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAGAGAGCTTAGACCTT 4800
QY 4801 TTCAATTTGCGAGGTAAACACCTGAACGACTACGGAGAAAACGTTTCAAGCTTCTCCTG 4860
Db 4801 TTCAATTTGCGAGGTAAACACCTGAACGACTACGGAGAAAACGTTTCAAGCTTCTCCTG 4860
QY 4861 CAACCTCATATCTCGACAGCTGTTACTGGGACCACAGGAGGCGCCCTTACTCAGATATTT 4920
Db 4861 CAACCTCATATCTCGACAGCTGTTACTGGGACCACAGGAGGCGCCCTTACTCAGATATTT 4920
QY 4921 GAGGACCACCTGAGGGCCCTGGATGACGAGGAGGAGGGTGAAGCATGAGGAGGAGTATGAT 4980
Db 4921 GAGGACCACCTGAGGGCCCTGGATGACGAGGAGGAGGGTGAAGCATGAGGAGGAGTATGAT 4980
QY 4981 GAAGATCCTCAGGTAGTGGGAAGTGAAGGGCGAGAGGAGGAGGAGGAGGAGTGAAGAG 5040
Db 4981 GAAGATCCTCAGGTAGTGGGAAGTGAAGGGCGAGAGGAGGAGGAGGAGGAGTGAAGAG 5040
QY 5041 GAGGACCTGAGTGGAGGGGACGAGGAGGATCAAGAGGTTTATACCATGAGAGGTTAGAT 5100
Db 5041 GAGGACCTGAGTGGAGGGGACGAGGAGGATCAAGAGGTTTATACCATGAGAGGTTAGAT 5100

QY 5101 GGCAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAAAGCGAAATGAGAA 5160
Db 5101 GGCAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAAAGCGAAATGAGAA 5160
QY 5161 CCTGAAGATGAGGGAAGATGATGACTAAGTAGAATAACCTATTTTGAAGAAATTCCTAT 5220
Db 5161 CCTGAAGATGAGGGAAGATGATGACTAAGTAGAATAACCTATTTTGAAGAAATTCCTAT 5220
QY 5221 TGTGATTTGACTGTTTTTACCCCATATCCCTCCCTCCCTCCCAATCCTGCCCCCTGAAACCT 5280
Db 5221 TGTGATTTGACTGTTTTTACCCCATATCCCTCCCTCCCTCCCAATCCTGCCCCCTGAAACCT 5280
QY 5281 ACTTTTTTCTGATTTGAACATTTCTCTGGAATGACACGGGAAAGTGTACTGGGGTTG 5340
Db 5281 ACTTTTTTCTGATTTGAACATTTCTCTGGAATGACACGGGAAAGTGTACTGGGGTTG 5340
QY 5341 TGGAGGAGGAGGCGGAGGCGGTGGACTAAATACCTATTTTACTGCCAAATAAAAT 5400
Db 5341 TGGAGGAGGAGGCGGAGGCGGTGGACTAAATACCTATTTTACTGCCAAATAAAAT 5400
QY 5401 AATATTTGTAATATTAATTAACCTGGGATAGTACTAGCTTTGTAGAATGATTACTATTAATTTCT 5460
Db 5401 AATATTTGTAATATTAATTAACCTGGGATAGTACTAGCTTTGTAGAATGATTACTATTAATTTCT 5460
QY 5461 CTCTCTCTTTTTATTTTTTACACATCTATTTCTTTTAAAGTATAGTCCCTTTAGTCCAAG 5520
Db 5461 CTCTCTCTTTTTATTTTTTACACATCTATTTCTTTTAAAGTATAGTCCCTTTAGTCCAAG 5520
QY 5521 GAAAGGCACTACAATCCACTTATTAATGCTTACTGTTCAAGTAAAAATAAGCTCC 5580
Db 5521 GAAAGGCACTACAATCCACTTATTAATGCTTACTGTTCAAGTAAAAATAAGCTCC 5580
QY 5581 AGATTTTACAAAAGAGGAGAAAGAAATATTTACAAATGAAATGTTGCTTAAAAATTTAA 5640
Db 5581 AGATTTTACAAAAGAGGAGAAAGAAATATTTACAAATGAAATGTTGCTTAAAAATTTAA 5640
QY 5641 ACAAAATACAGTAAATGATTTGTTAAAGCAAAATCTATTTTAAAAATTTTAAATAAGA 5700
Db 5641 ACAAAATACAGTAAATGATTTGTTAAAGCAAAATCTATTTTAAAAATTTTAAATAAGA 5700
QY 5701 AATAATTTGCTTAAAGCAAAATTTTGGAAAAATAAATGCACCTTTTACTTGTATTTAT 5760
Db 5701 AATAATTTGCTTAAAGCAAAATTTTGGAAAAATAAATGCACCTTTTACTTGTATTTAT 5760
QY 5761 TATTAACAATGATTTATAAGCTT 5785
Db 5761 TATTAACAATGATTTATAAGCTT 5785

RESULT 3
AAA88237
ID AAA88237 standard; DNA; 1035 bp.
XX AAA88237;
XX AC
XX XX
DT 15-DEC-2000 (first entry)
XX Human variant pp32rl nucleotide sequence.
XX
KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
XX malignant; cytostatic; gene therapy; ds.
OS Homo sapiens.
XX
PN WO200045852-A1.
XX
PD 10-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US02656.
XX
PR 03-FEB-1999; 99US-0118667.

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XX (UYJO ) UNIV JOHNS HOPKINS.
PA Pasternack GR, Bai J;
XX P-PSDB; AAB20655.
DR WPI; 2000-514896/46.
XX P-PSDB; AAB20655.
PT Treatment of cancer comprising restoration of pp32 function in
PT malignant cells -
XX Example 3; Fig 3; 90pp; English.
XX The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human variant pp32r1 nucleotide sequence from
CC an example of the present invention.
XX Sequence 1035 BP; 322 A; 189 C; 308 G; 216 T; 0 other;
SQ
Query Match 17.9%; Score 1035; DB 21; Length 1035;
Best Local Similarity 100.0%; Pred. No. 7.9e-150;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4357 GAGTCTTCAAAAGTCTAAACGCTGGCGCGTTCGAGGTTTATTGATTGAATTCGGC 4416
DB 1 GAGTCTTCAAAAGTCTAAACGCTGGCGCGTTCGAGGTTTATTGATTGAATTCGGC 60
QY 4417 TGGCAGCAGAGGCTCTGCAGACAGAGAGCGCGAGAGATGGAGATGGCAGCGGATTTCAT 4476
DB 61 TGGCAGCAGAGGCTCTGCAGACAGAGAGCGCGAGAGATGGAGATGGCAGCGGATTTCAT 120
QY 4477 TCAGAGCTCGGAACAGCGCGCCCTCTGATGTGAAGAACTTGCCTCGACAACTAGTCGG 4536
DB 121 TCAGAGCTCGGAACAGCGCGCCCTCTGATGTGAAGAACTTGCCTCGACAACTAGTCGG 180
QY 4537 TCGAATGAAGGCAAACTCGAAGCCCTCAGAGATGAATTTGAAGAACTTGAAGTCTTAAGT 4596
DB 181 TCGAATGAAGGCAAACTCGAAGCCCTCAGAGATGAATTTGAAGAACTTGAAGTCTTAAGT 240
QY 4597 AAAATCAAGCGAGGCTCACCTCAATCTCAGACTTACCAAAAGTTAAAGTTGAGAAAGCTT 4656
DB 241 AAAATCAAGCGAGGCTCACCTCAATCTCAGACTTACCAAAAGTTAAAGTTGAGAAAGCTT 300
QY 4657 GAACTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCAT 4716
DB 301 GAACTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCAT 360
QY 4717 CTATATTAAAGTGGCAACAAATTAAGACCTCAGCACAATAGACCACTGAACAGTTA 4776
DB 361 CTATATTAAAGTGGCAACAAATTAAGACCTCAGCACAATAGACCACTGAACAGTTA 420
QY 4777 GAAAACCTCAAGAGCTTAGACCTTTTCAATTGGAGGTAAACCAACCTGAACACTACGGA 4836
DB 421 GAAAACCTCAAGAGCTTAGACCTTTTCAATTGGAGGTAAACCAACCTGAACACTACGGA 480
QY 4837 GAAAACGTGTTCAAGCTTCTCGCAACTCAGATATCTCGACAGCTGTTACTGGACACAC 4896
DB 481 GAAAACGTGTTCAAGCTTCTCGCAACTCAGATATCTCGACAGCTGTTACTGGACACAC 540
QY 4897 AAGGAGGCGGCTTACTCAGATATTGAGGACCACTGAGGGGCTGATGACGAGGAGGAG 4956
DB 541 AAGGAGGCGGCTTACTCAGATATTGAGGACCACTGAGGGGCTGATGACGAGGAGGAG 600
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QY 4957 GGTGAGCATGAGGAGGATGATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGCGCGAG 5016
DB 601 GGTGAGCATGAGGAGGATGATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGCGCGAG 660
QY 5017 GAGGAGGAGGAGGAGGATGAAGAGGAGGAGGCTGAGTGGAGGGGACGAGGAGGATGAAGAA 5076
DB 661 GAGGAGGAGGAGGAGGATGAAGAGGAGGAGGCTGAGTGGAGGGGACGAGGAGGATGAAGAA 720
QY 5077 GGTATTAACCATGAGAGGTAGATGGCAGAGAGATGAAGAAGAGCTTGTGTGAAGAGAA 5136
DB 721 GGTATTAACCATGAGAGGTAGATGGCAGAGAGATGAAGAAGAGCTTGTGTGAAGAGAA 780
QY 5137 AGGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5196
DB 781 AGGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 5197 TAACCTATTGTAAGAAATTCCTATTGATGATTTGACTGTTTACCCATATCCCTCCCTCC 5256
DB 841 TAACCTATTGTAAGAAATTCCTATTGATGATTTGACTGTTTACCCATATCCCTCCCTCC 900
QY 5257 CTCCAATCTGCGCCCTGAAACTTACTTTTCTGATTTGTAACATTTGCTGTGGAATGAG 5316
DB 901 CTCCAATCTGCGCCCTGAAACTTACTTTTCTGATTTGTAACATTTGCTGTGGAATGAG 960
QY 5317 ACGGGAAGGAGTACTGGGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5376
DB 961 ACGGGAAGGAGTACTGGGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 5377 ACTATTTTACTGCC 5391
DB 1021 ACTATTTTACTGCC 1035
RESULT 4
AA81537
ID AA81537 standard; DNA; 889 BP.
XX
AC AA81537;
XX AC
XX AC
DT 26-AUG-1999 (first entry)
XX
DE Genomic sequence of phosphoprotein 32 variant pp32r2.
XX
XX Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;
KW prostatic adenocarcinoma; antineoplastic activity;
KW transformation suppression; malignant potential; neuroendocrine;
KW neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.
XX
OS Homo sapiens.
XX
XX WO9929906-A2.
XX
XX 17-JUN-1999.
XX
XX 11-DEC-1998; 98WO-US26433.
XX
XX 12-DEC-1997; 97US-0069677.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Brody JR, Kadkol SS, Kochevar GJ, Pasternack GR;
XX
XX WPI; 1999-385626/32.
XX
XX Phosphoprotein 32 (pp32) related genomic sequences
XX
XX Claim 1; Fig 5; 65pp; English.
XX
XX The present sequence represents the genomic sequence of phosphoprotein
CC 32 (pp32) variant pp32r2. The pp32r1 and pp32r2 sequences are associated
CC with cancer in prostate, especially prostatic adenocarcinomas. Normal
CC pp32 exerts antineoplastic activity through suppression of
CC transformation. Cancer-associated pp32 variants augment, rather than
```

CC inhibit, transformation. Determining the presence of a gene encoding
CC residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a
CC diagnostic method for predicting malignant potential of neuroendocrine,
CC neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.
XX
SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 15.4%; Score 889; DB 20; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCTCTGCAGACAGAGAGCGC 4447
DB 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCTCTGCAGACAGAGAGCGC 60

QY 4448 GAGAGATGGAGTGGCAGACGGATTTCATTCAGAGCTCGGAAACAGAGCGGCCCTCTGATG 4507
DB 61 GAGAGATGGAGTGGCAGACGGATTTCATTCAGAGCTCGGAAACAGAGCGGCCCTCTGATG 120

QY 4508 TGAAGAAGACTTGGCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAG 4567
DB 121 TGAAGAAGACTTGGCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAG 180

QY 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 4627
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240

QY 4628 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGCGCTCGAAGTAT 4687
DB 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGCGCTCGAAGTAT 300

QY 4688 TGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGAAC 4747
DB 301 TGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGAAC 360

QY 4748 TCAGCACAAATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATT 4807
DB 361 TCAGCACAAATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATT 420

QY 4808 GCGAGGTAAACAACCTGAACGACTACGAGAAACAGTTCCTCAAGCTTCTCTGCAACTCA 4867
DB 421 GCGAGGTAAACAACCTGAACGACTACGAGAAACAGTTCCTCAAGCTTCTCTGCAACTCA 480

QY 4868 CATATCTCGACAGCTGTACTGGACACACAAAGAGGCCCTTACTAGATATTGAGGACC 4927
DB 481 CATATCTCGACAGCTGTACTGGACACACAAAGAGGCCCTTACTAGATATTGAGGACC 540

QY 4928 ACCTGGAGGGCTCGATGACGAGGAGGGGTGAGCATGAGGAGGAGTATGATCAAGATG 4987
DB 541 ACCTGGAGGGCTCGATGACGAGGAGGGGTGAGCATGAGGAGGAGTATGATCAAGATG 600

QY 4988 CTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGTGAAGAGGAGGACG 5047
DB 601 CTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGTGAAGAGGAGGACG 660

QY 5048 TGAGTGGAGGGGACGAGGAGTGAACAAGTTTATACAGTGGAGAGGTAGATGGCGAGG 5107
DB 661 TGAGTGGAGGGGACGAGGAGTGAACAAGTTTATACAGTGGAGAGGTAGATGGCGAGG 720

QY 5108 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGCTCAGAACGCAAAATGAGAACCTGAAG 5167
DB 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGCTCAGAACGCAAAATGAGAACCTGAAG 780

QY 5168 ATGAGGAGAGATGATGACTTAAGTAACTATTTTGAAGAAATTCCTATTGTGATT 5227
DB 781 ATGAGGAGAGATGATGACTTAAGTAACTATTTTGAAGAAATTCCTATTGTGATT 840

QY 5228 TGACTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 5276
DB 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 889

RESULT 5

AAA88239
ID AAA88239 standard; DNA; 889 BP.
XX
AC AAA88239;
XX
DT 15-DEC-2000 (first entry)
XX
DE Human variant pp32r2 genomic DNA sequence.
XX
KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200045852-A1.
XX
PD 10-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US02656.
XX
PR 03-FEB-1999; 99US-0118667.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA
PI Pasternack GR, Bai J;
XX
XX WPI; 2000-514896/46.
DR
XX Treatment of cancer comprising restoration of pp32 function in
PT malignant cells -
XX
PS Example 5; Fig 5; 90pp; English.
XX
CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human variant pp32r2 genomic DNA sequence from
CC an example of the present invention.
XX
SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 15.4%; Score 889; DB 21; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCTCTGCAGACAGAGAGCGC 4447
DB 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCTCTGCAGACAGAGAGCGC 60

QY 4448 GAGAGATGGAGTGGCAGACGGATTTCATTCAGAGCTCGGAAACAGAGCGGCCCTCTGATG 4507
DB 61 GAGAGATGGAGTGGCAGACGGATTTCATTCAGAGCTCGGAAACAGAGCGGCCCTCTGATG 120

QY 4508 TGAAGAAGCTTGGCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAG 4567
DB 121 TGAAGAAGCTTGGCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAG 180

QY 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 4627
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240

QY 4628 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGCGCTCGAAGTAT 4687
DB 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGCGCTCGAAGTAT 300

Db	781	GGTGAAGAAGAAAGGGGTCAAGACGAAACGAAACCTGAAGATGAGGAGAGATGAT	840
Qy	5185	GACTAAGTAGAATAAACCTATTTTGAAAAATTCCTATTGTGATTGACTGTTTACCCAT	5244
Db	841	GACTAAGTGGANAATACCTATTTTGAAAAATTCCTATTGTGATTGACTGTTTACCCAT	900
Qy	5245	ATCCCCCT-----CCCCCTCCCAATCTCGCCCTGAAACTTACTTTTCTGATTGTAA	5298
Db	901	ATCCCCCTCTCCCCCCCCCTCTATCTCTGCCCCCTGAACTTATTTTCTGATTGTAA	960
Qy	5299	CATTGCTGTGGGAATGAGCGGGAATGTACTGGGGTGTGGAGGAGGAGGCGAG	5358
Db	961	CGTTCGTGTGGACAGAGAGGGGAAGAGTGACTGCGGGTTCGCGGGGA-GGATGCGGG	1019
Qy	5359	GAGCGGTGGACTAAAATACTATTTTACTGCC	5391
Db	1020	GTGGGGTGGAAATAAATACTATTTTACTGCC	1052
RESULT 8			
AAx81536			
ID	AAx81536 standard; DNA; 1052 BP.		
XX	AAx81536;		
AC	26-AUG-1999 (first entry)		
XX	Nucleotide sequence of normal human phosphoprotein 32 (pp32).		
DE	Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;		
XX	prostatic adenocarcinoma; antineoplastic activity;		
KW	transformation suppression; malignant potential; neuroendocrine;		
KW	neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	WO9929906-A2.		
PN	17-JUN-1999.		
PD	11-DEC-1998; 98WO-US26433.		
XX	12-DEC-1997; 97US-0069677.		
PF	(UWJO) UNIV JOHNS HOPKINS.		
XX	Brody JR, kadkol SS, Kocheavar GJ, Pasternack GR;		
PI	WPI; 1999-385626/32.		
XX	Phosphoprotein 32 (pp32) related genomic sequences		
DR	Example 2; Fig 3; 65pp; English.		
PT	The present sequence represents a human phosphoprotein 32 (pp32)		
XX	nucleotide sequence. The specification describes pp32 variants,		
CC	designated pp32r1 and pp32r2. The pp32r1 and pp32r2 sequences are		
CC	associated with cancer in prostate, especially prostatic adenocarcinomas.		
CC	Normal pp32 exerts antineoplastic activity through suppression of		
CC	transformation. Cancer-associated pp32 variants augment, rather than		
CC	inhibit, transformation. Determining the presence of a gene encoding		
CC	residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a		
CC	diagnostic method for predicting malignant potential of neuroendocrine,		
CC	neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.		
XX	Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;		
QS			
Query Match 15.0%; Score 867.8; DB 20; Length 1052;			
Best Local Similarity 91.8%; Pred. No. 3.1e-124; Indels 19; Gaps 4;			
Matches 967; Conservative 0; Mismatches 67;			
Qy	4357	GATCTTCAAAAGTCTCAAAAGTGCGCGCGTGGTTCGAGGTTTATTGATTGAATCGGC	4416

AA88238	standard; DNA; 1052 BP.
AAA8238;	
15-DEC-2000	(first entry)
Human pp32	nucleotide sequence.
Human; pp32;	chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
acidic protein	rich in leucine; chromosome 15q25; tumour suppressor;
malignant;	cytostatic; gene therapy; ds.
Homo sapiens.	
WO200045852-A1.	
10-AUG-2000.	
03-FEB-2000;	2000WO-US02656.
03-FEB-1999;	99US-0118667.
(UIJO)	UNIV JOHNS HOPKINS.
Pasternack GR,	Bai J;
WPI; 2000-514896/46.	
P-PSDB; AAB20656.	
Treatment of cancer	comprising restoration of pp32 function in
malignant cells -	
Example 3; Fig 3;	90pp; English.
The present invention	describes a method (M1) for treating malignant
cells comprising	restoration of pp32 function. Also described are:
(1) a method (M2)	of screening to determine whether a compound is an
inducer of pp32	expression comprising measuring pp32 expression by
cells cultured in	the presence and absence of the compound; and
(2) a method (M3)	of screening to determine whether a compound is an
inducer of pp32	function comprising measuring protein phosphatase
activity in cells	cultured in the presence and absence of the compound.
The methods are	useful for treating cancer and for identifying agents
which may be used	to treat cancer. Human pp32 is a phosphoprotein which
has been mapped	to chromosome 15q22.3-q23. The present sequence
represents the	human pp32r1 nucleotide sequence from an example of
the present	invention.
Sequence 1052	BP; 326 A; 196 C; 316 G; 214 T; 0 other;
Query Match	15.0%; Score 867.8; DB 21; Length 1052;
Best Local Similarity	91.8%; Pred. No. 3.1e-124;
Matches 967;	Conservative 0; Mismatches 67; Indels 19; Gaps 4;
QY 4357	GAGCTCTTCAAAAGTCTCTAAACGTCGGCGCGTGGGTTTATTGATGAATTCGGC 4416
Db 1	GAATTCCTAAAGTCTCTAAACGTCGGCGCGTGGGTTTATTGATGAATTCGGC 60
QY 4417	TGGCAGGAGGCTCTGCAGACAGAGAGCGCGAGAGATGGAGATGGCGACGGATTCA 4476
Db 61	CGCGCGGGAGGCTCTGCAGAGAGAGAGCGCGAGATGGAGATGGCGACGGATTCA 120
QY 4477	TCAGAGCTCGGAACAGGGCCCTCTGATGTGAAGAACTTCCTCTGACACACAGTCGG 4536
Db 121	TTAGAGCTCGGAACAGAGCCCTCTGATGTGAAGAACTTCCTCTGACACACAGTCGG 180
QY 4537	TGCAATGAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTTGAATTCCTTA 4596
Db 181	TGCAATGAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTTGAATTCCTTA 240
QY 4597	AAATCAACGAGGAGGCTCACTCAATCTCAGACTTACCAAGTTA---AAGTTGAGAAG 4653
Db 241	ACAATCAAGTAGGCTCACTCAATCGCAAACTTACCAAGTTAACAACAACTTAAGAAG 300

OS Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -

XX Claim 1; SEQ ID No 995; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;

CC (4) treating (M5) an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis, renal
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection, and
CC parasitic infection, protozoal infection, fungal infection, and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;

Query Match 15.0%; Score 867.8; DB 24; Length 1052;

Best Local Similarity 91.8%; Pred. No. 3.1e-124;

Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTAAAGTCCATAAACGTCGGCGCGGTCGGGTTTATGATTAATTCGC 4416

Db 1 GAAATCCCAAGTCCATAAACGTCGGCGCGGTCGGGTTTATGATTAATTCGC 60

QY 4417 TGGCAGCAGAGCCTCTGCAGACAGAGCGCGGAGAGATGAGATGGCAGCGGATTCAT 4476

Db 61 CGGCGGGAGGACCTCTGCAGAGAGAGCGCGGAGAGATGAGATGGCAGCGGATTCAT 120

QY 4477 TCAGAGCTGCGGAACACAGGGCGCCCTCTGATGTGAAGAAGAACTTCCCTGGACAAACATCGG 4536
Db 121 TTAGAGCTGCGGAACACAGGGCGCCCTCTGATGTGAAGAAGAACTTCCCTGGACAAACATCGG 180
QY 4537 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTCAAGAACTGGAATTTCTTAAGT 4596
Db 181 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTCAAGAACTGGAATTTCTTAAGT 240
QY 4597 AAAATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAAAGTTA---AAGTTGAGAAAG 4653
Db 241 ACAATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAAAGTTA---AAGTTGAGAAAG 300
QY 4654 CTTGAACCTA-----AGAGTCTCAGGGGCGCTTGAAGTATTTGGCAGAAAAAGTCTCCG 4704
Db 301 CTTGAACCTAAGGATTAACAGAGTCTCAGGGGCGCTTGAAGTATTTGGCAGAAAAAGTCTCCG 360
QY 4705 AACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCA 4764
Db 361 AACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCA 420
QY 4765 CTGAACACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCAACCTG 4824
Db 421 CTGAACACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCAACCTG 480
QY 4825 AACGACTACGAGGAGAAACGTTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 4884
Db 481 AACGACTACGAGGAGAAACGTTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 540
QY 4885 TACTGGACACACAGGAGGCGCCCTTACTCAGATATTTAGGACACCTGAGGAGGCGCTTGGAT 4944
Db 541 GACCGGACACACAGGAGGCGCCCTTACTCAGATATTTAGGACACCTGAGGAGGCGCTTGGAT 600
QY 4945 GACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATCAAGATGCTCAGGTAGTGGAGAT 5004
Db 601 GATGAGGAGGAGGTGAGCATGAGGAGGAGTATGATCAAGATGCTCAGGTAGTGGAGAT 660
QY 5005 GAGGAGGCGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGGAGTGTAGTGGAGGAGGAG 5064
Db 661 GAGGAGGCGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGGAGTGTAGTGGAGGAGGAG 720
QY 5065 GAGGATGAAGAGGTTTAAAGTGGAGGAGTATGATCGGAGGAGGAGTGAAGAGGAGCTT 5124
Db 721 GAGGATGAAGAGGTTTAAAGTGGAGGAGTATGATCGGAGGAGGAGTGAAGAGGAGCTT 780
QY 5125 GGTGAAGAAAGAGGGTTCAGAACGCGAAATGAGAACCTGGAAGATGAGGAGGAGGAGATGAT 5184
Db 781 GGTGAAGAAAGAGGGTTCAGAACGCGAAATGAGAACCTGGAAGATGAGGAGGAGGAGATGAT 840
QY 5185 GACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATTTGACTGTTTACCCTAT 5244
Db 841 GACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATTTGACTGTTTACCCTAT 900
QY 5245 ATCCCTCT-----CCCCCTCCAACTCTCCCTGAACTTACTCTTTTCTGATTTCTAA 5298
Db 901 ATCCCTCTCTCCCCCTCCAACTCTTAATCTCCCTGAACTTACTCTTTTCTGATTTCTAA 960
QY 5299 CATTCGTGTGGGAATGAGACGCGGAAAGTGTACTGTGGGGTGTGGAGGAGGAGGAGGAG 5358
Db 961 CGTTGCTGTGGGAATGAGACGCGGAAAGTGTACTGTGGGGTGTGGAGGAGGAGGAGGAG 1019
QY 5359 GAGCGGTGGACTAAATACTATTTTACTGCC 5391
Db 1020 GTGGGGGTGGAATAAAATACTATTTTACTGCC 1052

RESULT 11

AAV71743

ID AAV71743 standard; cdna; 916 BP.

XX AAV71743;

XX AAV71743;

DT 15-MAR-1999 (first entry)

XX		Human V3 loop HIV receptor P30/PHAPI cDNA.
DE		
XX		
KW		HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;
KW		P30 protein; PHAPI; Infection; therapy; diagnosis; ss.
XX		
OS		Homo sapiens.
XX		
FH		Key Location/Qualifiers
FT	CDS	104..853
FT		/*tag= a
XX		
PN		WO9804080-A1.
XX		
PD		17-SEP-1998.
XX		
PF		12-MAR-1998; 98WO-EP01409.
XX		
PR		12-MAR-1997; 97US-0040969.
XX		
PA		(CNRS) CENT NAT RECH SCI.
PA		(INSP) INST PASTEUR.
XX		
PI	Briand J, Callebaut C, Guichard G, Hovanessian A;	
PI	Jacotot E, Krust B, Muller S;	
XX		
DR	WPI; 1999-034588/03.	
DR	P-PSDB; AAW84053.	
XX		
PT	New isolated V3 loop HIV receptor - comprises p95/nucleolin,	
PT	P40/PHAPII and P30/PHAPI proteins, used to develop products for the	
PT	treatment and prevention of HIV infection	
XX		
PS	Claim 17; Fig 49(12); 267pp; English.	
XX		
CC	This cDNA sequence codes for the P30 (or PHAPI) protein of the	
CC	newly identified V3 loop HIV receptor. This novel protein complex	
CC	receptor for HIV retroviruses consists of an association of 3	
CC	proteins named p95/nucleolin, p40/PHAPII and p30/PHAPI (see	
CC	AAW84053-54). These proteins were isolated from human CD4+ CEM	
CC	T-cell extracts using an affinity matrix containing either the	
CC	pseudopeptide 5(KpsICH2NPR)-template assembled synthetic peptide	
CC	or a synthetic V3 loop peptide (see AAW84055). P30 was identified	
CC	as PHAPI by amino acid sequence analysis. The invention also	
CC	concerns peptidic or non-peptidic molecules having the ability to	
CC	alter and/or prevent the binding of the novel HIV receptor to the	
CC	HIV retrovirus, and to pharmaceutical and diagnostic compositions	
CC	containing such molecules. Methods are provided for screening for	
CC	new active molecules, and to methods of screening genetic defects	
CC	in the expression of the V3 loop HIV receptor in individuals that	
CC	survive long-term HIV infection or who are HIV-resistant. Such	
CC	genetically defective polynucleotides can be used in gene therapy.	
XX		
SQ	Sequence 916 BP; 296 A; 167 C; 275 G; 178 T; 0 other;	
	Query Match 13.7%; Score 791; DB 20; Length 916;	
	Best Local Similarity 93.2%; Pred. No. 1.8e-112;	
	Matches 853; Conservative 0; Mismatches 50; Indels 12; Gaps	
QY	4350 GCTGGTTGAGTCTTCAAAGTCTTAACAGTCGGCGCGGTTCGAGTTATTGATGA 4409	
Dd	1 GCTGGTTGAGCCTTCAAGTCTTAAACGCGCGCGGTTCGGGTTTTATTGATGA 60	
QY	4410 ATTTCGGCTGGCAGGAGGCTCTGCAGACAGAGCGCGCAGATGGAGATGGCGACACG 4469	
Dd	61 ATTCGCCGGCGGGAGGCTCTGCAGAGAGAGCGCGGAGATGGAGATGGCGACACG 120	
QY	4470 GATTCAATTCAGAGCTCGGAACAGCGCGCCTCTCATGTGAAAGAACAATGCGCTGGACAA 4529	
Dd	121 GATTCAATTTAGAGCTCGGAACAGGACGCCCTCTGATCTGAAAGAACAATGTCCTGGACAA 180	
QY	4530 CAGTCGGTGCAGTAGAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACAATGGAATT 4589	

Query Match		11.2%;	Score 649.6;	DB 17;	Length 980;
Best Local Similarity		83.0%;	Pred. No. 8e-91;		
Matches 807;		Conservative	0;	Mismatches 144;	Indels 21; Gaps 5;
Qy	4437	ACAGAGAGCGGAGAGATGGAGATGGCGACAGCGGATTCATTACAGAGCTGCGGAACAGGCG	4496		
Db	10	AGAGAGAGCGGAGAGATGGAGATGGCAACAGGATTTATTAGAGCTGCGGAACAGGAC	69		
Qy	4497	GCCCTCTGATGTGAAGAACTTGCCTGGACACACAGCTCGTCAATGAAGGCAAACTCGA	4556		
Db	70	GCCCTCTGATGTGAAGAGCTGGCCCTGGATAACTGTAAGTCAATTAAGGCAAAATCGA	129		
Qy	4557	AGCCCTCACAGATGAATTTGAAGAACTTGAAGTAAATCAACGAGGCGCTCAC	4616		
Db	130	AGGCCTCACGGATGAGTTTGAGAACTTGAATTCCTAAGTACAATCAACGTAGGCCTCAC	189		
Qy	4617	CTCAATCTCAGACTTACCAAGTTA-----AAGTTGAGAAAGCTTGAACTA-----AG	4664		
Db	190	CTCAATTTCCAACCTTACCAAGTTTAAACAAACTCAAGAAGCTTGAATTAAGCGGAAACAG	249		
Qy	4665	AGTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATT	4724		
Db	250	AATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCATCTAAATTT	309		
Qy	4725	AAGTGGCAACAAATTAAGACCTTCAGCACATAGAGCCACTGAAACAGTTAGAAACCT	4784		
Db	310	AAGTGGCAACAAATAAGATCTCAGCACATAGAGCCGCTGAAGAAGTTAGAGATCT	369		
Qy	4785	CAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCACTCAAGCACTACGAGAAACGT	4844		
Db	370	CAAGAGCTTAGACCTTTTAACTGTGAGGTGACCAACCTGAATGCCTTACCGAATAACGT	429		
Qy	4845	GTTCAACTTCTCTGCAACTCACAATTCGACAGCTGTTACTGGACACACAAGAGGC	4904		
Db	430	GTTCAACTCTCTGCCCGAGTCTATGTACCTCGATGCGTATGACAGGGGACACAAGAGGC	489		
Qy	4905	CCCTTACTCAGATATTGAGGACACACGTGGAGGCGCTTGGATGAGGAGGAGGTCAGCA	4964		
Db	490	CCCGACTCCGACTTGGAGGCTACGTGA-----GGATCAGCAGCAGGAAGATGAGGA	543		
Qy	4965	TGAGGAGGATGATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGA	5024		
Db	544	TGAGGAGGATGATGATGAATATGCCAGCTAGTGGAGATGAAGAGATGAAGAGGTTGAGGA	603		
Qy	5025	GGAGGAGCTCAAGAGAGACGTGAGTGGAGGGACGAGGAGGATGAAGAGGTTATAA	5084		
Db	604	GGAGGAGGGGAGGAGAGGATGTGATGGAGAGGAGGAGGATGAGGAAGGTTACAA	663		
Qy	5085	CGATGGAGAGGTAGATGGCGGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTCA	5144		
Db	664	TGACGGGAAGTGGATGACGAGGAGACGACGAAGAGAGCTGGTGAAGAGAGGGAGTCA	723		
Qy	5145	GAAGCGAAATGAGAACTTCAAGATGAGGAGAGAGATGATGACTAAGTAAGTAACCTAT	5204		
Db	724	GAAGCGAAATGAGAACTTCAAGATGAGGAGAGAGATGATGACTAAGTAAGTAACCTAT	782		
Qy	5205	TTTCAAAATTCCTATTGTGATTTGACTGTTTTACCATATCCCTCCCTCCCAATC	5264		
Db	783	TTGGGAAATTCCTATTGTGATTTGACTGTTTTACCATATCCCTCCCTCCCTATTTC	842		
Qy	5265	CTGCCCCCTGAAACTTACTTTTTTCTGATTGTTAATCTGCTGTGGAAATGAGACGGAAA	5324		
Db	843	CTGCCCCCTGAAACTTACTTTTTTCTGATTGTAGCATTTGCTGTGGGAGGAGGGGAAA	902		
Qy	5325	AGTGTACTGGGGTTG--TGGAGGGAGGGAGGCGAGGCGGTGGACTAAAATACTATT	5382		
Db	903	AGTGTACTGGGGTTGATGATGGGGTGGGGTGGGGGAGGGGTGGNAATAAATACTATT	962		
Qy	5383	TTTACTGCCAAA	5394		
Db	963	TTTACTGCCACA	974		

RESULT 14	
AB199657	AB199657 standard; cDNA; 980 BP.
XX	AC AB199657;
XX	DT 07-MAR-2002 (first entry)
XX	Mouse ischaemic condition related cDNA sequence SEQ ID NO:687.
DE	XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX	KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX	OS Mus musculus.
XX	PN WO20018188-A2.
XX	PD 22-NOV-2001.
XX	PF 18-MAY-2001; 2001WO-JP04192.
XX	PR 18-MAY-2000; 2000JP-0145977.
XX	PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX	PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX	DR WPI; 2002-034733/04.
XX	P-PSDB; ABB57251.
XX	Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes -
XX	Claim 2; Page 1714-1716; 2690pp; English.
XX	The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
XX	Sequence 980 BP; 312 A; 169 C; 302 G; 197 T; 0 other;

Query Match		11.2%;	Score 649.6;	DB 24;	Length 980;
Best Local Similarity		83.0%;	Pred. No. 8e-91;		
Matches 807;		Conservative	0;	Mismatches 144;	Indels 21; Gaps 5;
Qy	4437	ACAGAGAGCGGAGAGATGGAGATGGCGACAGCGGATTCATTACAGAGCTGCGGAACAGGCG	4496		
Db	10	AGAGAGAGCGGAGAGATGGAGATGGACAAACGGATTTATTAGAGCTGCGGAACAGGAC	69		
Qy	4497	GCCCTCTGATGTGAAGAACTTGCCTGGACACACAGTGGTCAATGAAGGCAAACTCGA	4556		
Db	70	GCCCTCTGATGTGAAGAGCTGCTCTGATAACTGTAAGTCAATTGAAGCAAAATCGA	129		
Qy	4557	AGCCCTCACAGATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCAC	4616		
Db	130	AGGCCTCAGGATGAGTTTGAAGAACTTGAATTCCTTAAGTACAATCAACGTAGGCCTCAC	189		
Qy	4617	CTCAATCTCAGACTTACCAAACTTA---AAGTTGAGAAAGCTTGAACTA-----AG	4664		

Db	301	AAAGACCTCAGCACAAATAGACCCACTGAAAAAGTTAGAAAAACCTCAAGAGGCTTAGACCTT	360
Qy	4801	TTCAATTGCGAGGTAACCAACCTGAACGACTACGGAGAAAACGTGTCAAGCTTCTCCTG	4860
Db	361	TTCAATTGCGAGGTAACCAACCTGAACGACTACGGAGAAAATGTTCAGGCTCCTCCCG	420
Qy	4861	CAACTCACATATCTCGACAGCTGTACTGGACCAACAGGAGGCCCTTACTCAGATATT	4920
Db	421	CAACTCACATATCTCGACGGCTATGACCGGACGACAAAGGAGGCCCTGACTCGGATGCT	480
Qy	4921	GAGGACCACTGGAGGGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGATATGAT	4980
Db	481	GAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGATATGAT	540
Qy	4981	GAAGATGCTCAGGTAGTGGAAAGATGAGGAGGGCGAGGAGGAGGAGGAGGTTGAAGAG	5040
Db	541	GAAGATGCTCAGGTAGTGGAAAGATGAGGAGGGCGAGGAGGAGGAGGAGGTTGAAGAG	600
Qy	5041	GAGGACGTGAGTGGAGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGAT	5100
Db	601	GAGGACGTGAGTGGAGGAGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGAT	660
Qy	5101	GGCGAGGAGAGATGAAGAAGACCTTGGTGAAGAAAGGGGTCAAGAAGGAAATGAGAA	5160
Db	661	GACGAGGAAGATGAAGAAGACCTTGGTGAAGAAAGGGGTCAAGAAGGAAATGAGAA	720
Qy	5161	CCTGAAGATGAGGAGAGATGATGACTAA	5190
Db	721	CCTGAAGATGAGGAGAGATGATGACTAA	750

Search completed: December 8, 2002, 15:13:19
Job time : 799 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 14:59:02 ; Search time 123 Seconds
(without alignments)
14423.781 Million cell updates/sec

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Perfect score: 5785
Sequence: 1 aagcttctcgtactctctaa.....aaacaatgatttaagctt 5785

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	867.8	15.0	1052	1	US-08-466-603-1
2	867.8	15.0	1052	1	US-08-314-503A-1
3	867.8	15.0	1052	1	US-08-468-066-1
4	867.8	15.0	1052	2	US-08-466-717-1
5	867.8	15.0	1052	3	US-08-466-743-1
6	867.8	15.0	1052	5	PCT-US95-12414-1
7	649.6	11.2	980	1	US-08-466-603-3
8	649.6	11.2	980	1	US-08-314-503A-3
9	649.6	11.2	980	1	US-08-468-066-3
10	649.6	11.2	980	2	US-08-466-717-3
11	649.6	11.2	980	3	US-08-466-743-3
12	649.6	11.2	980	5	PCT-US95-12414-3
13	508	8.8	759	1	US-08-466-603-4
14	508	8.8	759	1	US-08-314-503A-4
15	508	8.8	759	1	US-08-468-066-4
16	508	8.8	759	2	US-08-466-717-4
17	508	8.8	759	3	US-08-466-743-4
18	508	8.8	759	5	PCT-US95-12414-4
19	326	5.6	387	4	US-09-018-584A-5
20	296.4	5.1	966	2	US-08-766-738-2
21	296.4	5.1	966	4	US-09-262-610-2
22	233	4.0	14636	4	US-09-173-914-6
23	232.6	4.0	162450	4	US-09-345-882-1
24	228.4	3.9	70000	4	US-09-851-896-3
25	228.4	3.9	84495	4	US-09-797-906-3
26	227.4	3.9	99500	4	US-09-798-096-10
27	226.6	3.9	713	4	US-08-943-607-23

28	226.6	3.9	713	4	US-08-943-607-24
29	226.6	3.9	6063	1	US-08-195-744-4
30	226.6	3.9	6063	2	US-08-788-279-4
31	226.6	3.9	59065	4	US-09-813-817-3
32	226.6	3.9	59065	4	US-09-978-197-3
33	226	3.9	28001	4	US-09-819-993-3
34	225	3.9	713	4	US-08-943-607-25
35	225	3.9	713	4	US-08-943-607-26
36	224.2	3.9	152331	3	US-09-128-155-16
37	223.4	3.9	5408	1	US-08-471-058-20
38	223.4	3.9	5408	3	US-08-471-057-20
39	223.2	3.9	111282	4	US-09-754-250-3
40	223	3.9	26664	4	US-09-564-805-28
41	221.8	3.8	87350	3	US-08-781-891-79
42	221.8	3.8	87543	4	US-09-791-211-3
43	221.4	3.8	2886	2	US-08-687-080-55
44	221.4	3.8	6330	4	US-09-880-427-2
45	221.4	3.8	6330	4	US-09-306-538B-2

ALIGNMENTS

RESULT 1
US-08-466-603-1
; Sequence 1, Application US/084666603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
US-08-466-603-1

```
Query Match          15.0%; Score 867.8; DB 1; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.7e-169;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAAGTCTTAAACGTCGGCGGCTTCAGAGTTTATTGATTGAATTCGCG 4416
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GAATTCCTCCAAAGTCTTAAACGTCGGCGGCTTCAGAGTTTATTGATTGAATTCGCG 60

QY 4417 TGGCAGCAGAGGCTCTGCACAGAGAGCGCGGAGAGATGGAGATGGCGAGCGGATTTCAT 4476
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CGCGCGGAGGCTCTGCAGAGAGAGAGCGCGGAGAGATGGAGATGGCGAGCGGATTTCAT 120

QY 4477 TCAGAGCTCGGAACAGAGCGCCCTCTGATGTGAAGAACTTGCCTCGACAACTAGTCGG 4536
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TTAGAGCTCGGAAACAGGAGCGCCCTCTGATGTGAAGAACTTGTCTCGACAACTAGTCGG 180

QY 4537 TCGAATGAAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTCCTTAAGT 4596
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TCGAATGAAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTCCTTAAGT 240

QY 4597 AAAATCAACGGAGGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 4653
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 ACATCAACGTAGGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 300

QY 4654 CTTGAACTA-----AGAGTCTCAGGGGCGCTTGAAGTATTGGCAGAAAGTGTCCA 4704
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 CTTGAACTAAGCGATAACAGAGTCTCAGGGGCGCTTGAAGTATTGGCAGAAAGTGTCCG 360

QY 4705 AACCTCAGCATCTATATTAAAGTGGCAACAAATTAAGACCTCAGCACATATAGAGCA 4764
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 AACCTCAGCATCTATATTAAAGTGGCAACAAATTAAGACCTCAGCACATATAGAGCA 420

QY 4765 CTGAACAGTATAGAAACCTCAAGAGCTTAGACCTTTCAATTCGAGGTACCAACCTG 4824
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 CTGAACAGTATAGAAACCTCAAGAGCTTAGACCTTTCAATTCGAGGTACCAACCTG 480

QY 4825 AAGGACTACGGAGAAACGTGTTCAGCTTCTCCTGCAACTCACATATCTCGACAGCTGT 4884
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 AAGGACTACGGAGAAACGTGTTCAGCTTCTCCTGCAACTCACATATCTCGACAGCTAT 540

QY 4885 TACTGGACCAACAGAGGCGCCCTTACTCAGATATTGAGGACCACTGGAGGCGCTGGAT 4944
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GACCGGGACGACAAGGAGCGCCCTGACTCGGATGTGAGGGCTACTGTGAGGCGCTGGAT 600

QY 4945 GACGAGGAGGAGGTGAGCATGAGGAGGATGATGAAGATGCTCAGTAGTGAAGAT 5004
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 GATGAGGAGGAGGATGAGCATGAGGAGGATGATGAAGATGCTCAGTAGTGAAGAT 660

QY 5005 GAGGAGGCGAGAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGTGGAGGGGACGAG 5064
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 GAGGAGGCGAGGATGAGGAGGAGGAGGAGTGAAGAGGAGGAGGAGGAGGAGGAG 720

QY 5065 GAGGATGAAGAGGTTATACGATGAGAGGTAGATGGCGAGGAGAGTCAAGAGAGCTT 5124
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 721 GAGGATGAAGAGGTTATACGATGAGAGGTAGATGGCGAGGAGAGTGAAGAGAGCTT 780

QY 5125 GGTGAAGAGAGAGGAGGTCAGAGCGAAATCAGAACCTTGAAGATGAGGAGAGAGATGAT 5184
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 781 GGTGAAGAGAGAGGAGGTCAGAGCGAAATCAGAACCTTGAAGATGAGGAGAGAGATGAT 840

QY 5185 GACTAAGTGAATPAACCTATTTTGAAAAATTCCTATTTGATTTGACTGTTTTTACCCTAT 5244
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 841 GACTAAGTGAATPAACCTATTTTGAAAAATTCCTATTTGATTTGACTGTTTTTACCCTAT 900

QY 5245 ATCCCTT-----CCCCCTTCAATCTCCCTCCCTGAAACTTACTTTTTCTGATGTGAA 5298
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 901 ATCCCTTCTCCCTCCCTTCAATCTCCCTCCCTGAAACTTACTTTTTCTGATGTGAA 960

QY 5299 CATTTGCTGGGAATCAGACGGGAAAGTGTACTGGGGGTTGTGGAGGAGGAGGGGAG 5358
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 961 CGTTGCTGTGGGACGAGGAGGAGAGTGTACTGGGGGTTGCGGGGGA--GGATGGCGG 1019

QY 5359 GAGGCGGTGGACTAAAATACTATTTTACTGCC 5391
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Db 1020 GTGGGGTGAATAAAATACTATTTTACTGCC 1052
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RESULT 2
US-08-314-503A-1
; Sequence 1, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated with
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-314-503A-1

Query Match          15.0%; Score 867.8; DB 1; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.7e-169;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAAGTCTTAAACGTCGGCGGCTTCAGAGTTTATTGATTGAATTCGCG 4416
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GAATTCCTCCAAAGTCTTAAACGTCGGCGGCTTCAGAGTTTATTGATTGAATTCGCG 60

QY 4417 TGGCAGCAGAGGCTCTGCACAGAGAGCGCGGAGAGATGGAGATGGCGAGCGGATTTCAT 4476
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CGCGCGGAGGCTCTGCAGAGAGAGAGCGCGGAGAGATGGAGATGGCGAGCGGATTTCAT 120

QY 4477 TCAGAGCTCGGAAACAGGCGCCCTCTGATGTGAAGAACTTGCCTCGACAACTAGTCGG 4536
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TTAGAGCTCGGAAACAGGCGCCCTCTGATGTGAAGAACTTGTCTCGACAACTAGTCGG 180

QY 4537 TCGAATGAAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTCCTTAAGT 4596
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TCGAATGAAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTCCTTAAGT 240

QY 4597 AAAATCAACGGAGGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 4653
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 241 ACAATCAACGTTAGGCGCTCACCTCAATCGCAAACTTACCAAGTTAAACAACCTTAAGAAG 300
QY 4654 CTTGAACHTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCA 4704
Db 301 CTTGAACHTAAGCGATACAGAGTCTCAGGGGCGCTAGAAGTATTGGCAGAAAAGTGTCCG 360
QY 4705 AACCTCAGGCATCTATATTTAAGTGGCAACAATAAAGAACCTTCAGCAATAGAGCCA 4764
Db 361 AACCTCAGGCATCTATATTTAAGTGGCAACAATAAAGAACCTTCAGCAATAGAGCCA 420
QY 4765 CTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAACCAACCTG 4824
Db 421 CTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAACCAACCTG 480
QY 4825 AACGACTACGGAGAAAACGTTCTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 4884
Db 481 AACGACTACGGAGAAAACGTTCTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 540
QY 4885 TACTGGGACCAAGAGGCGCCCTTACTCAGATATTGAGGACCACTGAGGGCCCTGGAT 4944
Db 541 GACCGGACGACAAAGAGGCGCCCTGACTCGATGCTGAGGCTACGTGGAGGCGCTGGAT 600
QY 4945 GACGAGGAGGAGGTGAGCATGAGGAGAGTATGATGATGATGATGATGATGATGATGAT 5004
Db 601 GATGAGGAGGAGGTGAGCATGAGGAGAGTATGATGATGATGATGATGATGATGATGAT 660
QY 5005 GAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5064
Db 661 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 5065 GAGGATCAACAGGTTATACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 5124
Db 721 GAGGATCAACAGGTTATACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 780
QY 5125 GGTGAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 5184
Db 781 GGTGAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 840
QY 5185 GACTAAGTAGAATAACCTATTTTGAATAATTCCTATTGTGATTTGACTGTTTTCACCCAT 5244
Db 841 GACTAAGTAGAATAACCTATTTTGAATAATTCCTATTGTGATTTGACTGTTTTCACCCAT 900
QY 5245 ATCCCTCTCC-----CCCTCCCTCAATCTGTCCTCCCTGAACTTACTTTTCTGATGATA 5298
Db 901 ATCCCTCTCCCTCCCTCCCTCTAATCTGTCCTCCCTGAACTTACTTTTCTGATGATA 960
QY 5299 CATGTGTGGGAATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5358
Db 961 CGTTGTGTGGGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1019
QY 5359 GAGCGGTGGACTAAATACTATTTTACTGCG 5391
Db 1020 GTGGGGGTGGAATAAATACTATTTTACTGCC 1052

RESULT 3

US-08-468-066-1
; Sequence 1, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated with
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,066
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 97..843
US-08-468-066-1

Query Match 15.0%; Score 867.8; DB 1; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.7e-169;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAACTCTATAAACGTCGGCGCTGGGTTCCGAGGTTTATGATTGAATTCGCG 4416
Db 1 GAATTCCTCAAACTCTATAAACGTCGGCGCTGGGTTTATGATTGAATTCGCG 60
QY 4417 TGGCAGGAGAGCCTCTGCAGACAGAGAGCGCGAGAGATGGAGATGGCAGAGGATTCAT 4476
Db 61 CGCGCGGAGAGCCTCTGCAGAGAGAGAGCGCGAGAGATGGAGATGGCAGAGGATTCAT 120
QY 4477 TCAGAGCTCGGAAACAGAGCGGCCCTCTCTGATGTGAAGAACTTGCCTCGAACAACAGTCGG 4536
Db 121 TTAGAGCTCGGAAACAGAGCGGCCCTCTCTGATGTGAAGAACTTGTCTCGAACAACAGTCGG 180
QY 4537 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTTGAATTTCTTAAGT 4596
Db 181 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTTGAATTTCTTAAGT 240
QY 4597 AAAATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 4653
Db 241 ACAATCAACGAGGCGCTCACCTCAATCGCAAACTTACCAAAAGTTAACAACAACTTAAGAAG 300
QY 4654 CTTGAACHTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCA 4704
Db 301 CTTGAACHTAAGCGATACAGAGTCTCAGGGGCGCTAGAAGTATTGGCAGAAAAGTGTCCG 360
QY 4705 AACCTCAGGCATCTATATTTAAGTGGCAACAATAAAGAACCTTCAGCAATAGAGCCA 4764
Db 361 AACCTCAGGCATCTATATTTAAGTGGCAACAATAAAGAACCTTCAGCAATAGAGCCA 420
QY 4765 CTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAACCAACCTG 4824
Db 421 CTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAACCAACCTG 480
QY 4825 AACGACTACGGAGAAAACGTTCTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 4884
Db 481 AACGACTACGGAGAAAACGTTCTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 540
QY 4885 TACTGGGACCAAGAGGCGCCCTTACTCAGATATTGAGGACCACTGAGGGCGCTGGAT 4944


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; Sequence 1, Application PC/TUS9512414
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: Novel Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12414
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoschelt Esq., Dale H.
; REGISTRATION NUMBER: 19,090
; REFERENCE/DOCKET NUMBER: 1107.51507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97...843
; PCT-US95-12414-1

Query Match 15.0%; Score 867.8; DB 5; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.7e-169;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTAAAGTCTAAACGTCGGCGGTTCGAGGTTTATTGATTGAATTCGGC 4416
Db 1 GAATTCCTCCAAAGTCCTAAACCGCGCGGTTCGAGGTTTATTGATTGAATTCGGC 60
QY 4417 TGGCAGGAGGCTCTGCAGACAGAGAGCGCGAGAGATGGAGATGGCAGACGGATTTCAT 4476
Db 61 CGGCGGGAGGCTCTGCAGACAGAGAGCGCGAGAGATGGAGATGGCAGACGGATTTCAT 120
QY 4477 TCAGAGCTCGGAACAGGCGGCCCTCTGATGTGAAGAACTTTCCTCGCAGCAACAGTCGG 4536
Db 121 TTAGAGCTCGGAACAGGAGCGCCCTCTGATGTGAAGAACTTTCCTCGCAGCAACAGTCGG 180
QY 4537 TCGAATGAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTGAATTCCTTAAGT 4596
Db 181 TCGAATGAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTGAATTCCTTAAGT 240
QY 4597 AAATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAACTTA---AAGTTGAGAAAG 4653
Db 241 ACATCAAGTAGGCGCTCACCTCAATCTCAGAACTTACCAAACTTAACCAAACTTAAGAG 300
QY 4654 CTTGAACATA-----AGAGTCTCAGGGGCGCTGGAAGTATTGCGAGAAAGTGTCCA 4704
Db 301 CTTGAACATAAGCGATAAACAGAGTCTCAGGGGCGCTAGAAAGTATTGGCAGAAAAGTGTCCG 360
QY 4705 AACCTCACGCATCTATATTTAAAGTGGCAACAAAATTAAGACCTCAGCACATAGAGCCA 4764
Db 361 AACCTCACGCATCTAAATTTAAAGTGGCAACAAAATTAAGACCTCAGCACATAGAGCCA 420
QY 4765 CTGAACACAGTTAGAAAACCTCAAGAGCTTAGAGCTTTTCAATTTGGAGGTAAACCACTG 4824
Db 421 CTGAACAAAGTTAGAAAACCTCAAGAGCTTAGAGCTTTTCAATTTGGAGGTAAACCACTG 480
QY 4825 AACGACTACGGAGAAACCTGTTCAAGCTTCTCCGCACTCACAATATCTCCACAGCTGT 4884
Db 481 AACGACTACCGAGAAATGTGTTCAAGCTTCTCCGCACTCACAATATCTCCACGCTAT 540
QY 4885 TACTGGGACCAAGAGGCGCCCTTACTCAGATATTGAGGACCACTGGAGGCGCTTGGAT 4944
Db 541 GACCGGACCAAGAGGCGCCCTGACTCGGATGCTGAGGGCTACGTGGAGGCGCTTGGAT 600
QY 4945 GACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGAT 5004
Db 601 GATGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGAT 660
QY 5005 GAGGAGGCGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGTGAAGAGGAGGAG 5064
Db 661 GAGGAGGAGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGTGAAGAGGAGGAG 720
QY 5065 GAGGATGAAGAGGTTTATAACGATGGAGAGTATGATGGGAGGAGGAGGAGTGAAGAGGAGT 5124
Db 721 GAGGATGAAGAGGTTTATAACGATGGAGAGTATGATGGGAGGAGGAGTGAAGAGGAGT 780
QY 5125 GGTGAAGAGAAAGGGGTCAAGACGCGAAATGAGACCTTGAAGATGAGGAGGAGGAGTATGAT 5184
Db 781 GGTGAAGAGAAAGGGGTCAAGACGCGAAATGAGACCTTGAAGATGAGGAGGAGGAGTATGAT 840
QY 5185 GACTAAGTGAATTAACCTATTTTGAATAATTCCTATTGTTGACTGTTTACCCAT 5244
Db 841 GACTAAGTGAATTAACCTATTTTGAATAATTCCTATTGTTGACTGTTTACCCAT 900
QY 5245 ATCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 5298
Db 901 ATCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 960
QY 5299 CATTCGTGTGGGAATGAGACGGGAAAGTCTACTGGGGTTGTGGAGGAGGAGGAGGAG 5358
Db 961 CGTTGCTGTGGGAACGAGGAGGAGGAGTCTACTGGGGTTGTGGAGGAGGAGGAGGAG 1019
QY 5359 GAGCGGTGAGCTAAATTAATTAATTTTACTGCC 5391
Db 1020 GTGGGGTGAATAAATACTATTTTACTGCC 1052

RESULT 7
US-08-466-603-3
; Sequence 3, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466, 603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314, 503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: mus sp
; US-08-466-603-3

Query Match 11.2%; Score 649.6; DB 1; Length 980;
Best Local Similarity 83.0%; Pred. No. 1.2e-124;
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;

QY 4437 ACAGAGCGCGAGAGATGGAGATGGCAGACGGGATTCATTACAGAGCTGGCGAAGCGGC 4496
DB 10 AGAGAGCGCGAGAGATGGAGATGGACAAACGGATTTATTAGAGCTGGCGAAGCGAC 69

QY 4497 GCCCTCTGATGTAAGAGACTGCGCTGGGCAACAGCTCGGTCGAATGAAGCAAACTCGA 4556
DB 70 GCCCTCTGATGTAAGAGACTGCGCTGGGTAACCTGAAGTCAATGAAGGCAAAATCGA 129

QY 4557 AGCCCTCACAGATGAATTTGAAGAACTGGAATCTTAAAGTAAATCAACGAGGCCCTCAC 4616
DB 130 AGGCCTCACAGATGAGTTGAAGAACTGGAATCTTAAAGTAAATCAACGAGGCCCTCAC 189

QY 4617 CTCATCTCAGACTTACCAAAAGTTA---AGTTGAGAAAGCTTGAACTA-----AG 4664
DB 190 CTCATTTTCCAACTTACCAAAAGTTTAAACAACTCAAGAAGCTTGAATTAAGCGAAACAG 249

QY 4665 AGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAGTGTCCAACTCAGCATCTACGATCTATATT 4724
DB 250 AATCTCAGGGGCGCTGGAAGTATTGGCAGAAAGTGTCCAACTCAGCATCTACGATCTATATT 309

QY 4725 AAGTGGCAACAAAATTAAAGACCTCAGCACAAATAGAGCCACTGAACAGATTAGAAAACCT 4784
DB 310 AAGTGGCAACAAAATTAAAGATCTCAGCACAAATAGAGCCGCTGAAGAAGTTAGAGATCT 369

QY 4795 CAAGAGCTTAGACCTTTTCAATTCGAGGATTAACCACTGAACGACTACGAGAGAAAACGT 4844
DB 370 CAAGAGCTTAGACCTTTTCAATTCGAGGATTAACCACTGAACGACTACGAGAGAAAACGT 429

QY 4845 GTTCAAGCTTCTCCTGCAACTCACATATCTCAGACGCTGTTACTGGGACCAACAGGAGGC 4904
DB 430 GTTCAAGCTTCTCCTGCAAGCTGATGTTACCTCGATGGGTATGACAGGCAACAGGAGGC 489

QY 4905 CCCTTACTCAGATATTGAGGACCACTGGAGGGCCTGACGACGAGGAGGGGTGAGCA 4964
DB 490 CCCGACTCCGATGTTGAGGCTACGTGGA-----GGATGACGACGAGGAGATGAGGA 543

QY 4965 TGAGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGA 5024
DB 544 TGAGAGGAGTATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603

QY 5025 GGAGGAAGGTCAAGAGGAGGAGCTGAGTGGGGGAGGAGGAGGAGGATGAAGAGGTTTAA 5084
DB 604 GGAAGAGGGGAGGAGGAGGAGGATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663

QY 5085 CGATGGAGAGGTAGATGGCGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCA 5144
DB 664 TGACGGGGAAGTGGATGACGAGGAGACGAGAGAGAGCTGGTGAAGAAGAGAGGGAGTCA 723

QY 5145 GAAGCGAAAATGAGAACCTGAAGATGAGGAGAGAGATGACTAAGTAGAATAACCTAT 5204
DB 724 GAAGCGAAAACGAGAACCGGAGATGAGGCGAAGAGGATGACTAAGGA-ATGAACCTGT 782

QY 5205 TTTGAAAAATTCCTATTGTGATTGACTGTTTTTACCCTATCCCTCCCTCCCTCAATC 5264
DB 783 TTGGGGAATTCCTATTGTGATTGACTGTTTTTACCCTATCCCTCCCTCCCTCAATC 842

QY 5265 CTGCCCCCTGAAACTTACTTTTTCTGATTGTAACATGCTGTGGAATGAGACGGGAAA 5324
DB 843 CTGCCCCCGAATCTATTTTTCTGATTGTAACATGCTGTGGAATGAGACGGGAAA 902

QY 5325 AGTGTACTGGGGTTG--TGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5382
DB 903 AGTGTACTGGGGTTGATGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGTGGGGGT 962

QY 5383 TTTTACTGCCAAA 5394
DB 963 TTTTACTGCCACA 974

RESULT 8
US-08-314-503A-3
; Sequence 3, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated with
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: mus sp
; US-08-314-503A-3

Query Match 11.2%; Score 649.6; DB 1; Length 980;
Best Local Similarity 83.0%; Pred. No. 1.2e-124;
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;

QY 4437 ACAGAGCGCGAGAGATGGAGATGGCGACAGCGGATTCATTAGAGCTGCGGAACAGGGC 4496
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QY 4497 GCCCTCTGATGTGAAGAACTTGCCTTGGGACAAACAGTCGGTCTGAATGAAGCGAAATCTGA 4556
Db 70 GCCCTCTGATGTGAAGAGCTTGCCTTGGATGAATGAATGAAGTCAATTTGAAGCGCAAAATCTGA 129
QY 4557 AGCCCTCAGATGAATTTGAAGAACTTGAATTTCTTAAAGTAAATCAACGAGCGCTCAC 4616
Db 130 AGGCTCAGGATGAGTTTGAAGAACTTGAATTTCTTAAAGTAAATCAACGAGCGCTCAC 189
QY 4617 CTCATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 4664
Db 190 CTCATTTCCAACTTACCAAAAGTTAACAACACTCAAGAGCTTGAATTAAGCGAAACAG 249
QY 4665 AGTCTCAGGGGCTTGAAGTATTGGCGAGAAAAGTGTCCAAACCTCAGCAATCTATATTT 4724
Db 250 AATCTCAGGGGACCTTGAAGTATTGGCGAGAAAAGTGTCCAAACCTCAGCAATCTATATTT 309
QY 4725 AAGTGGCAACAAAATTAAGAGCTTGAAGTATTGGCGAGAAAAGTGTCCAAACCTCAGCAATCTATATTT 4784
Db 310 AAGTGGCAACAAAATTAAGAGCTTGAAGTATTGGCGAGAAAAGTGTCCAAACCTCAGCAATCTATATTT 369
QY 4845 GTTCAAGCTTCTCCTGCAACTCAGATCTGAGAGCTTGTACCTGAGGAGGAGGAGGAGG 4904
Db 430 GTTCAAGCTTCTCCTGCAACTCAGATCTGAGAGCTTGTACCTGAGGAGGAGGAGGAGGAGG 489
QY 4905 CCTTACTCAGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4964
Db 490 CCTTACTCAGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 543
QY 4965 TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGG 5024
Db 544 TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGG 603
QY 5025 GGAGGAAGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5084
Db 604 GGAGGAAGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663
QY 5085 CGATGAGAGGTAGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5144
Db 664 TGACGGGAAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
QY 5145 GAAGCGAAAATGAGAACTTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5204
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QY 5205 TTTGAAAATTCCTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 5264
Db 783 TTTGAAAATTCCTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 842
QY 5265 CTGCCCCCTGAACTTACTTTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 5324
Db 843 CTGCCCCCTGAACTTACTTTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 902
QY 5325 AGTGTACTGGGGGTTG---TGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5382
Db 903 AGTGTACTGGGGGTTG---TGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
QY 5383 TTTTACTGCCAAA 5394
Db 963 TTTTACTGCCACA 974

RESULT 9
US-08-468-066-3
; Sequence 3, Application US/08468066
; Patent No. 5756676

GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,066
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
; ORGANISM: mus sp
US-08-468-066-3
Query Match 11.2%; Score 649.6; DB 1; Length 980;
Best Local Similarity 83.0%; Pred. No. 1.2e-124;
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;
QY 4437 ACAGAGCGCGAGAGATGGAGATGGCGACAGCGGATTCATTAGAGCTGCGGAACAGGGC 4496
Db 10 AGAGAGCGCGAGAGATGGAGATGGCGACAAACGCGATTTATTAGAGCTGCGGAACAGGAC 69
QY 4497 GCCCTCTGATGTGAAGAACTTGCCTTGGGACAAACAGTCGGTCTGAATGAAGCGAAATCTGA 4556
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QY 4785 CAAGAGCTTATGAGCTTTTCAATTTGCGAGGTAACCAACCTGAACTACGAGGAGGAGGAGGAGGAGG 4844
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QY 4965 TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5024
Db 544 TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 603
QY 5025 GGAGGAAGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5084
Db 604 GGAGGAAGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663
QY 5085 CGATGAGAGGTAGATGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5144
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Db 724 GAAGCGAAAATGAGAACTTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
QY 5205 TTTGAAAATTCCTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 5264
Db 783 TTTGAAAATTCCTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 842
QY 5265 CTGCCCCCTGAACTTACTTTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 5324
Db 843 CTGCCCCCTGAACTTACTTTTCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 902
QY 5325 AGTGTACTGGGGGTTG---TGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5382
Db 903 AGTGTACTGGGGGTTG---TGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
QY 5383 TTTTACTGCCAAA 5394
Db 963 TTTTACTGCCACA 974

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Db 370 CAAGAGCCTAGACCTGTTTAACTGTGAGGTGACCAACCTGAACTGCCCTACCGAGAAACGT 429
QY 4845 GTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGTACTGGGACACACAGGAGGC 4904
Db 430 GTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGTACTGGGACACACAGGAGGC 489
QY 4905 CCCTTACTCAGATATTGAGGACCACTGGAGGCTGGATGACGAGGAGGAGGTGAGCA 4964
Db 490 CCCCGACTCCGATGTTGAGGCTACGTGGA-----GGATGACGACGAGGAATGAGGA 543
QY 4965 TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGAGGCGGAGGAGGAGGA 5024
Db 544 TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGAGGCGGAGGAGGTGAGGA 603
QY 5025 GGAGGAAGGTGAAGAGGAGCTGACTGAGGAGGAGGAGGAGGAGGATGAAGAGGTTATAA 5084
Db 604 GGAAGAAGGGGAGGAAGAGGATGTGAGTGAGGAGGAGGAGGAGGATGAGGAAGGTTACAA 663
QY 5085 CGATGGAGAGTATGATGCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCA 5144
Db 664 TGACGGGGAAGTGGATGACGAGGAAGACGAGGAAGAGCTGGTGAAGAAGAGGGAGTCA 723
QY 5145 GAACGGAAGTGAAGACCTGAAGATGAGGAGGAGGAAGATGACTAAGTGAAGTAACCTAT 5204
Db 724 GAACGGAAGTGAAGACCTGAAGATGAGGAGGAGGAGGAGGATGACTAAGGA-ATGAACCTGT 782
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Db 783 TTGGGGAATTCCTATTGTGATTTGACTGTTTTTACCCATATCCCTCCCTCCCTCCCTATT 842
QY 5265 CTGCCCCCTGAAACTTACTTTTTCTGATGTAACATTTGCTGGGAATGAGACGCGGAAA 5324
Db 843 CTGCCCCCTGAAACTTACTTTTTCTGATGTAACATTTGCTGGGAATGAGACGCGGAAA 902
QY 5325 AGTCTACTGGGGTTG--TGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5382
Db 903 AGTCTACTGGGGTTGATGGGGGTTGGGGGTTGGGGGTTGGGGGTTGGGAATAAATACTATT 962
QY 5383 TTTACTGCCAAA 5394
Db 963 TTTACTGCCCA 974
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RESULT 10
US-08-466-717-3
: Sequence 3, Application US/08466717
: Patent No. 5874234
: GENERAL INFORMATION:
: APPLICANT: Pasternack, Gary R.
: TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
: TITLE OF INVENTION: Uncontrolled Cell Division
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner, Birch, McKie & Beckett
: STREET: 1001 G Street, N.W.
: CITY: Washington, D.C.
: STATE: District of Columbia
: COUNTRY: U.S.A.
: ZIP: 20001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,717
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/314,503
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
```

```
: NAME: Posorske Esq., Laurence H.
: REGISTRATION NUMBER: 34,698
: REFERENCE/DOCKET NUMBER: 1107,47218
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202 508-9153
: TELEFAX: 202 508-9299
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 980 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: mus sp
: US-08-466-717-3
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Query Match 11.2%; Score 649.6; DB 2; Length 980;
Best Local Similarity 83.0%; Pred No. 1.2e-124;
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;

QY 4437 ACAGAGAGCGGAGAGATGGAGATGGGACGAGCGGATTCATTTCAGAGCTCGGAACAGGGC 4496
Db 10 AGAGAGAGCGGAGAGATGGAGATGGGACAAACGGATTTATTATTAGAGCTCGGAACAGGAC 69
QY 4497 GCCTCTGATGTGAAGAAGACTTGCCTCGACACACAGTCGGTGAATGAAGGCAAACTCGA 4556
Db 70 GCCTCTGATGTGAAGAAGCTGCTCGGATAAAGTAACTGTAAGTCAATTAAGGCAAAATCGA 129
QY 4557 AGCCCTCACAGATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCAC 4616
Db 130 AGCCCTCACGATGATTTGAAGAACTGGAATTCCTTAAGTCAATCAACGTAAGGCTCAC 189
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Db 250 AATCTCAGGGGACCTGGAAGTATTGGCAGAAAAGTGTCCGAACCTTAAGCATCTAAATTT 309
QY 4725 AAGTGCACAAATAATTAAGACCTCAGCAACATAGAGCCACTGAAACAGTTAGAAAACCT 4784
Db 310 AAGTGCACAAATAATAAGATCTCAGCACATAGAGCCGCTGAAGAAGTTAGACAATCT 369
QY 4785 CAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCACTGAAACGACTACGGAGAAAACGT 4844
Db 370 CAAGAGCCTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCTTACCGAGAAAACGT 429
QY 4845 GTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGTACTGGGACACACAGGAGGC 4904
Db 430 GTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGTACTGGGACACACAGGAGGC 489
QY 4905 CCCTTACTCAGATATTGAGGACCACTGGAGGCTGGATGACGAGGAGGAGGTGAGCA 4964
Db 490 CCCCGACTCCGATGTTGAGGCTACGTGGA-----GGATGACGACGAGGAATGAGGA 543
QY 4965 TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGA 5024
Db 544 TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAAGAGGAGGAGGTTGAGGA 603
QY 5025 GGAGGAAGGTGAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGGTTATAA 5084
Db 604 GGAAGAAGGGGAGGAGGAGGATGTGAGTGAGGAGGAGGAGGAGGAGGAGGAGGTTACAA 663
QY 5085 CGATGGAGAGGTAGATGCGGAGGAAGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCA 5144
Db 664 TGACGGGGAAGTGGATGACGAGGAAGACGAGGAAGAGCTGGTGAAGAAGAGGAGGAGTCA 723
QY 5145 GAACGGAAGTGAAGACCTGAAGATGAGGAGGAGGAAGATGACTAAGTGAAGTAACCTAT 5204
Db 724 GAACGGAAGTGAAGACCTGAAGATGAGGAGGAGGAGGAGGAGGATGACTAAGGA-ATGAACCTGT 782
```


;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 1001 G Street, N.W.
;; CITY: Washington, D.C.
;; STATE: District of Columbia
;; COUNTRY: U.S.A.
;; ZIP: 20001
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/12414
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/314,503
;; FILING DATE: 22-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hoscheit Esq., Dale H.
;; REGISTRATION NUMBER: 19,090
;; REFERENCE/DOCKET NUMBER: 1107.51507
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202 508-9153
;; TELEFAX: 202 508-9299
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 980 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; ORIGINAL SOURCE: mus sp
;; ORGANISM: mus sp
PCT-US95-12414-3

Query Match 11.2%; Score 649.6; DB 5; Length 980;
Best Local Similarity 83.0%; Pred. No. 1.2e-124;
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;

QY 4437 ACAGAGCGCGAGAGATGGGACAGCGATTCATTACAGAGCTCGGGAACAGGCG 4496
Db 10 AGAGAGCGCGAGAGATGGGACAGCGATTCATTACAGAGCTCGGGAACAGGCG 69
QY 4497 GCCTCTGATGTAAGAAGTTCCTCTGACACACAGTTCGATGAAGGAAACAGCGA 4556
Db 70 GCCTCTGATGTAAGAAGTTCCTCTGACACACAGTTCGATGAAGGAAACAGCGA 129
QY 4557 AGCCCTCAGAGTGAATTTGAAGAACTGGAATTCCTTAAGTAACTCAAGAGGCTGCTAC 4616
Db 130 AGCCCTCAGAGTGAATTTGAAGAACTGGAATTCCTTAAGTAACTCAAGAGGCTGCTAC 189
QY 4617 CTCATCTCAGACTTACCAAGTGA---AAGTTGAGAAAGCTTGAAGT-----AG 4664
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QY 4665 AGTCTCAGGGGCTGGAAGTATTGCGAAGAAAGTTCGAACCTGACGATCTATATTT 4724
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QY 4725 AAGTGGCAACAAATTAAGACCTCAGCAATAGAGCCACTGAAACAGTGAAGAACT 4784
Db 310 AAGTGGCAACAAATTAAGACCTCAGCAATAGAGCCACTGAAACAGTGAAGAACT 369
QY 4785 CAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACACCTGACGAGTACGGAAGAACT 4844
Db 370 CAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACACCTGACGAGTACGGAAGAACT 429
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Db 430 GTTCAAGCTTCCTGCAACTACATATCTGACAGCTGTTACTGGGACCAAGAGGCG 489

QY 4905 CCTTACTCAGATATTGAGGACCAGCTGGAGGGCCCTGGATGACGAGGAGGAGGTGAGCA 4964
Db 490 CCCGACTCCGATGTTGAGGGCTACGTGGA-----GGATGACGAGGAGGAGATGAGGA 543
QY 4965 TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGA 5024
Db 544 TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGG 603
QY 5025 GGAGGAAGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5084
Db 604 GGAAGAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663
QY 5085 CCATGGAGAGGTAGATGCGGAGGAGAGATGAAGAAGAGCTTGGTGAAGAGAAAGGGGTCA 5144
Db 664 TGACGGGGAAGTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
QY 5145 GAAGCGAAATGAGAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5204
Db 724 GAAGCGAAATGAGAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
QY 5205 TTGAAAAATTCCTATTGATGTTGACTGTTTACCATATCCCTCCCTCCCTCCCTCAATC 5264
Db 783 TTGGGAAATTCCTATTGATGTTGACTGTTTACCATATCCCTCCCTCCCTCCCTCAATC 842
QY 5265 CTGCCCCCTGAACTTACTTTTCTGATGTTGACTGTTTACCATATCCCTCCCTCCCTCAATC 5324
Db 843 CTGCCCCCTGAACTTACTTTTCTGATGTTGACTGTTTACCATATCCCTCCCTCCCTCAATC 902
QY 5325 AGTGACTGGGGGTTG--TGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5382
Db 903 AGTGACTGGGGGTTG--TGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
QY 5383 TTTACTGCCAA 5394
Db 963 TTTACTGCCAA 974

RESULT 13
US-08-466-603-4
; Sequence 4, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary P.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299


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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-466-603-4

Query Match      8.8%; Score 508; DB 1; Length 759;
Best Local Similarity 83.3%; Pred. No. 1.4e-95;
Matches 615; Conservative 0; Mismatches 115; Indels 8; Gaps 3;

QY 4657 GAACCTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCAGCGAT 4716
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QY 5377 ACTATTTTACTGCCAAA 5394
Db 736 ACTATTTTACTGCCACA 753

RESULT 14
US-08-314-503A-4
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; Sequence 4, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-314-503A-4

Query Match      8.8%; Score 508; DB 1; Length 759;
Best Local Similarity 83.3%; Pred. No. 1.4e-95;
Matches 615; Conservative 0; Mismatches 115; Indels 8; Gaps 3;

QY 4657 GAACCTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCAGCGAT 4716
Db 24 GAAACACAGATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCAT 83
QY 4717 CTATATTTAAGTGGCAACAAAATAAAGACCTCAGCACATAGAGCCACTGAACAGTTA 4776
Db 84 CTAATATTTAAGTGGCAACAAAATAAAGATCTCAGCACATAGAGCCGCTGAAGAAGTTA 143
QY 4777 GAAACACCTCAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGGA 4836
Db 144 GAGAATCTCAAGAGCCTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCTTACCGA 203
QY 4837 GAAACCTGTTTCAAGCTTCTCTGCACTACATATCTCGACAGCTGTTTACTGGGACCAAC 4896
Db 204 GAAACCTGTTTCAAGCTTCTCTGCACTACATATCTCGACAGCTGTTTACTGGGACCAAC 263
QY 4897 AAGGAGGCCCTTACTCAGATATTGAGGACCACTGAGGGCCCTGGATGACGAGGAGGAG 4956
Db 264 AAGGAGGCCCTTACTCAGATATTGAGGACCACTGAGGGCCCTGGATGACGAGGAGGAG 317
QY 4957 GGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGTAGTGAAGATGCTGAGGAGGAGGAG 5016
Db 318 GATGAGGATGAGGAGGAGTATGATGAATATGCCAGCTAGTGGAGAGATGAAGAGGAGGAG 377
```


Result No.	8			9		Description
	Score	Query Match	Length	DB	ID	
C 1	326	5.6	387	10	US-09-784-423-5	Sequence 5, Appli
C 2	245.6	4.2	22889	9	US-09-860-670-164	Sequence 164, App
C 3	242.2	4.2	9384	10	US-09-764-860-835	Sequence 835, App
C 4	237.6	4.1	25423	10	US-09-764-855-193	Sequence 193, App
C 5	237.6	4.1	25424	10	US-09-764-855-194	Sequence 194, App
C 6	235.6	4.1	13046	10	US-09-764-870-595	Sequence 595, App
C 7	234.8	4.1	167343	10	US-09-962-436-281	Sequence 281, App
C 8	234.8	4.1	167343	10	US-09-964-824-273	Sequence 273, App
C 9	234	4.0	12452	10	US-09-764-877-3989	Sequence 3989, Ap
C 10	232.8	4.0	99014	10	US-09-880-107-3428	Sequence 3428, Ap
C 11	232.4	4.0	174493	10	US-09-804-471A-3	Sequence 3, Appli
C 12	231.6	4.0	7927	10	US-09-764-877-2311	Sequence 2311, Ap
C 13	231.4	4.0	337	10	US-09-764-877-3785	Sequence 3785, Ap
C 14	230.8	4.0	7683	10	US-09-764-847-1173	Sequence 1173, Ap
C 15	230.6	4.0	3813	10	US-09-764-877-3325	Sequence 3325, Ap
C 16	230.6	4.0	23432	10	US-09-764-869-1332	Sequence 1332, Ap
C 17	230.6	4.0	148567	10	US-09-801-876B-3	Sequence 3, Appli
C 18	230.4	4.0	33795	10	US-09-880-107-2184	Sequence 2184, Ap
C 19	229.8	4.0	57130	10	US-09-835-081-3	Sequence 3, Appli


```

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAllo
; CURRENT APPLICATION NUMBER: US/09/764,855
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 193
; LENGTH: 25423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-855-193

```

Query Match 4.1%; Score 237.6; DB 10; Length 25423;
Best Local Similarity 85.7%; Pred. No. 7.4e-26;
Matches 276; Conservative 0; Mismatches 44; Indels 2; Gaps 1;

QY	655	TTCAATGTATAAAATCAGTCTTTGGCGGCGCACGGTGCTCACACCTATAATCCAGCACT	714
Db	4770	TACAATAATATAAAAATTAGTGTGCCGGGTACGGTGGCTACACCTGTAAATCCCAGCACT	4711
QY	715	TTGGGAGTCCCCAGCGCGGGGTCTACGAGGTCAAGAGATGAGACCATCATGTGCACAACAT	774
Db	4710	TTGGGAGGCCAAGGTGCAGCGATCAGAGGTCAAGAGATCAAGACCATCTTGGCCAACAT	4651
QY	775	GSTGAACCCCTGTCTACTATTAATACAAAAAATTATCTGGGTGTGGTCGCACATGCC	834
Db	4650	GGTGAACCCCAACTCTACTAAAAATAC--AAAAATTAACCTGGGCGTGATGGCATGTGCC	4593
QY	835	TGTAATCCCAACTACTTAGGAGGCGCTGAGCGAGGAATCGGTTGAACCTGGGAGCGCGAG	894
Db	4592	TGTAGTCCCAAGCTACTTCGGGAGGCTGAGGCAGGAAATCGCTTGAACCTGGGAGTGGAG	4533
QY	895	GTTCGAGTCAGCCGAGATCGCACCAATTGCATCCAGCCTGCACACAGACGAGACTCCAT	954
Db	4532	GTTCGAATGAGCCGAGATCGCACCACTGCATCCAGCCTGCAACAGAACAAGCACTCCGT	4473
QY	955	CCCAAACAAAAACAAACAAA	976
Db	4472	CTCAAAAAAAAAAAAAAGAAAA	4451

RESULT 5

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US-09-764-855-194/c
; Sequence 194, Application US/09764855
; Patent No. US20020119919A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P110
; CURRENT APPLICATION NUMBER: US/09764.855
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 194
; LENGTH: 25424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-855-194

```

Query Match 4.1%; Score 237.6; DB 10; Length 25424;
Best Local Similarity 85.7%; Pred. No. 7.4e-26;
Matches 276; Conservative 0; Mismatches 44; Indels 2; Gaps 1;

Qy	655	TTCAATGTAAAAAATCAGTCTTGGCCGGCGACGGTGGCTACACCTATATATCCAGCACT	714
Db	4772	TACAAAATATATAAAATTAGTGGCCGGGTACGGTGGCTACACCTGTAATCCAGCACT	4713
Qy	715	TTGGGAGTCCCCAGCGGGCGGTACAGAGTCAAGAGATGGAGACCATCATGGCCAACAT	774
Db	4712	TTTGGAGGCCAAGGTGGACGGATACAGAGTCAAGAGATCAAGACCATCTGGCCAAACAT	4653

Qy	775	GGTGAACCCCTGTCTCTACTATATAAATACAAAAAATATCTGGGTCTGGTGCACATGCC	834
Db	4652	GGTGAACCCCACTCTACTTAAAAATAC--AAAAATTAACCTGGCGCTGATGSCATGTGCC	4595
Qy	835	TGTAATCCCAACTACTATGGAGGCTCAGCGAGGAGNAATCGCTTTGAACCTGGGAGCGCGAG	894
Db	4594	TGTAATCCCAAGCTACTCTGGAGGCTCAGCGAGGAGNAATCGCTTTGAACCTGGGAGGTGGAG	4535
Qy	895	GTTCCAGTGAAGCCGAGATCCACCATTTGCACCTTCACGCTTGGCAACAGACGAGACTCCAT	954
Db	4534	GTTCCATGAGCCGAGATCGACCACTGCACCTTCAGCTTGGCAACAGACAGACTCCGT	4475
Qy	955	CCCAAAACAAACAAAAACAAA	976
Db	4474	CTCAAAAAAAAAAAAAAGAAAA	4453

RESULT 6

```

US-09-764-870-595/c
; Sequence 595, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 595
; LENGTH: 13046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-595

```

Query Match 4.1%; Score 235.6; DB 10; Length 13046;
Best Local Similarity 83.2%; Pred. No. 1.3e-25;
Matches 268; Conservative 0; Mismatches 54; Indels 0; Gaps 0

Qy	655	TTCATTTGTAATAATCAGTCTTTGGCGGCACGGTGGCTCACACCTATAATCCAGCACT	714
Db	2729	TTAGCTTTAAAGAAAAAAGTTGGCGGCACGGTGGCTCACACCTGTAAATCCAGCACT	2670
Qy	715	TTGGGAGTCCAGCGGGGGGTTCAGGAGTCAAGAGATGGAGACCATCATGTGGCCAAACAT	774
Db	2669	TTGGGAGGCTTGGCGCAGGAGAGATCAGGAGTCAAGAGATCGAGACCATCTAGGCAACAT	2610
Qy	775	GGTGAACCCCTGCTCTACTATATAATACAAAAAATTTCTGGGTGGTGGCGACATGCC	834
Db	2609	GGTGAACCCCGTCTCTACTATAAATAACAAAAAATTTAGCTGGGCGTGGTGGCGCAGGCC	2550
Qy	835	TGTAATCCCAACTACTAGGAGGAGCTGAGCGAGGAGAAATCGCTTGAACCTGGGAGGCGGAG	894
Db	2549	TGTAGTCCCAAGTACTCTGGAGGCTGAGCGGGAGAAATCGCTTGAACCCAGGAAAGAGAA	2490
Qy	895	GTTGCGAGTGAGCCGAGATCGACCCATTGCACTCCAGCCTGGCAACAGAGCGAGACTCCAT	954
Db	2489	GTTGCGACTGAGCCCAAGATTGTGCCTAGCTCCAGCTCCAGCCTGGCGACAGAGCGAGGCTCCGT	2430
Qy	955	CCCAAAACAAAAACAAAAA	976
Db	2429	CTCAAAATTTAATAATAATAAA	2408

RESULT 7

```

US-09-962-436-281
; Sequence 281, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Dete
; TITLE OF INVENTION: Sets

```

```
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962.436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 281
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-281

Query Match      4.1%; Score 234.8; DB 10; Length 167343;
Best Local Similarity 75.5%; Pred. No. 2.2e-25;
Matches 305; Conservative 0; Mismatches 97; Indels 2; Gaps 1;

QY 601 ACATGCTCTGACTACTGCTACAAATAGCCTCCCAACTCTTTGCTCTACTTAAATTCATT 660
DB 71422 ATAACTGTTGTTTTTCACGGAAGCAGTGGTTTCCAAATGTTTTTAATCATGTAAATCCATCA 71481
QY 661 GTAAAAAATCAGTCTTTGGCGGCGAGGTGGCTCACACCTTATAATCCAGCACTTTGGGA 720
DB 71482 GTAAAAAACAATTTAAGCTGGGTGGCTCACACCTGTAAATCCAGCACTTTGGGA 71541
QY 721 GTCCAGGCGGCGGTTCAGAGGTCAAGAGATGGAGACCATCATGCGCCAAACATGGTGA 780
DB 71542 GGCCAAAGGCGGCAGATCAGAGGTCAAGAGATCGAGAGCAGCCTGGCCAAACATGGTGA 71601
QY 781 ACCCTGCTCTACTATAATAACAAAAAATATCTGGGTGGTGGCGACATGCTCTGAAT 840
DB 71602 ACCCTTCTCTAGTAAAAAT--ATAAAAAATTAGCGGGGGTGGTGGCACGCGCTATAGT 71659
QY 841 CCCAACTACTAGGAGGCTGAGCGAGAGAAATCGCTTGAACCTGGGAGCGGAGGTTGCA 900
DB 71660 CCCAGCTACTCAAGAGACTGAGCGAGAGAAATCGCTTGAACCGGGAGCGAGGTTGCA 71719
QY 901 GTGAGCGGAGATCGACCACTTCACCTCCAGCTGGCAACAGAGCGAGACTCCATCCCAA 960
DB 71720 GTGAGCGGAGATGGACCACTGCACCTCCAGCTGACCAAGAGCGAGACTCCATCTCAA 71779
QY 961 ACAAAACAAAACAAACCATTGTAACATGCTGTGTAACATCT 1004
DB 71780 AAAAGAAACAAAACCAATTTAAGACTGCATCCCAATATATTT 71823

RESULT 8
US-09-964-824A-273
; Sequence 273, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-273
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Query Match      4.1%; Score 234.8; DB 10; Length 167343;
Best Local Similarity 75.5%; Pred. No. 2.2e-25;
Matches 305; Conservative 0; Mismatches 97; Indels 2; Gaps 1;

QY 601 ACATGCTCTGACTACTGCTACAAATAGCCTCCCAACTCTTTGCTCTACTTAAATTCATT 660
DB 71422 ATAACTGTTGTTTTTCACGGAAGCAGTGGTTTCCAAATGTTTTTAATCATGTAAATCCATCA 71481
QY 661 GTAAAAAATCAGTCTTTGGCGGCGAGGTGGCTCACACCTTATAATCCAGCACTTTGGGA 720
DB 71482 GTAAAAAACAATTTAAGCTGGGTGGCTCACACCTGTAAATCCAGCACTTTGGGA 71541
QY 721 GTCCAGGCGGCGGTTCAGAGGTCAAGAGATGGAGACCATCATGCGCCAAACATGGTGA 780
DB 71542 GGCCAAAGGCGGCAGATCAGAGGTCAAGAGATCGAGAGCAGCCTGGCCAAACATGGTGA 71601
QY 781 ACCCTGCTCTACTATAATAACAAAAAATATCTGGGTGGTGGCGACATGCTCTGAAT 840
DB 71602 ACCCTTCTCTAGTAAAAAT--ATAAAAAATTAGCGGGGGTGGTGGCACGCGCTATAGT 71659
QY 841 CCCAACTACTAGGAGGCTGAGCGAGAGAAATCGCTTGAACCTGGGAGCGGAGGTTGCA 900
DB 71660 CCCAGCTACTCAAGAGACTGAGCGAGAGAAATCGCTTGAACCGGGAGCGAGGTTGCA 71719
QY 901 GTGAGCGGAGATCGACCACTTCACCTCCAGCTGGCAACAGAGCGAGACTCCATCCCAA 960
DB 71720 GTGAGCGGAGATGGACCACTGCACCTCCAGCTGACCAAGAGCGAGACTCCATCTCAA 71779
QY 961 ACAAAACAAAACAAACCATTGTAACATGCTGTGTAACATCT 1004
DB 71780 AAAAGAAACAAAACCAATTTAAGACTGCATCCCAATATATTT 71823

RESULT 9
US-09-764-877-3989
; Sequence 3989, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3989
; LENGTH: 12452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3989

Query Match      4.0%; Score 234; DB 10; Length 12452;
Best Local Similarity 82.2%; Pred. No. 2.3e-25;
Matches 281; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 635 AACCTTTGTCCTACTTAAAAATTCATTGTAAAAAATCAGTCTTGCCCGGCGACGCTGCTC 694
DB 4966 AACCCCATCTCTACTAAAAATATACAAAAAAGGCGCCAGCACGCTTGGCTC 5025
QY 695 ACACCTATAATCCAGCACTTTGGGAGTCCAGCGGCGGGTCCAGAGTCAAGAGATG 754
DB 5026 ACACCTGTAATCCAGCACTTTGGGAAGCGGCGGAGATCAGGAGTCAGAGATC 5085
QY 755 GAGACCATCATGGCCAAACATGGTGAACCCCTGCTCTACTATAAAATACAAAAAATATATC 814
DB 5086 GAGACCATCTGGCTAAATGGTGAACCCCGCTGTACTTAAAAATACAAAAAATATAGC 5145
QY 815 TGGGTGTGGTGGCACATGCCTGTAAATCCCAACTACTAGGAGGCTGAGGAGGAGATCG 874
DB 5146 CAGGAGTGGTGGCAGGTGCCTGTAGTCCAGCTACTTTGGGAGGCTGAGGAGGAGATGG 5205
QY 875 CTTGAACCTGGGAGCGGAGGTTGCAGTGCAGCCGAGATCGACCATTTGCATCCAGCCT - 933
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; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match      4.0%; Score 232.4; DB 10; Length 174493;
Best Local Similarity 87.5%; Pred. No. 4.9e-25;
Matches 266; Conservative 0; Mismatches 36; Indels 2; Gaps 1;

QY 673 TCTTGGCGGGCAGCGTGGCTCACACCTATATATCCAGCACCTTTGGGAGTCCAGCGGG 732
Db 119476 TATGGGCTGGGCACAGTGGCTCACACCTGTATATCCAGCACCTTTGGGAGCGGCGAGCAGG 119417

QY 733 CGGGTCACGAGGTCAAGAGATGGAGACCATCATGGCCAAACATGGTGAAACCCCTGTCTCTA 792
Db 119416 CGGATCACAAGGTCAAGAGATCGAGACCACCCCTGGCCACACATGGTGAAACCCCGTCTTTA 119357

QY 793 CTATAAATCAAAAAATTTATCTGGGTGTGGTGGCACATGCCTGTAATCCCAACTACTAG 852
Db 119356 CTAAAAATAC--AAAAATTAGCTGGGCATGGTGGTGCATGGCTGTAGTCCAGCTACTCG 119299

QY 853 GGAGGCTGAGGCAGGAGAATCGTTGAACCTGGGAGGCGGAGGTTCAGTGGAGCGGAGAT 912
Db 119298 GGAGGCTGAGGCAGGAGAATCTTGAACCCGGGAGGAGAGGTTGCAGTGGAGCTGAGAT 119239

QY 913 CGCACCATTTGCACCTCCAGCTGGCAACAGAGCGAGACTCCATCCCAAAAAACAAAAAC 972
Db 119238 CACACCACCTGCACCTCCAGCTGGCAACAGAGCGGAGACTCCTTCTAAAAAANAANA 119179

QY 973 AAAA 976
Db 119178 AAAA 119175

RESULT 12
US-09-764-877-2311
; Sequence 2311, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2311
; LENGTH: 7927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2311

Query Match      4.0%; Score 231.6; DB 10; Length 7927;
Best Local Similarity 85.7%; Pred. No. 4.8e-25;
Matches 269; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 664 AAAATCACTCTTGGCGGCGAGGTGGCTCACACCTATATATCCAGCACCTTTGGGAGTC 723
Db 3019 AAAATAAATGGTTGGCGGCGGCTCACACCTGTATATCCAGCATTTTGGGAGGC 3078

QY 724 CCAGGCGGCGGCTCACAGAGTCAAGAGATGGAGACCATCATGGCCAAACATGGTGAAAC 783
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; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match      4.0%; Score 232.4; DB 10; Length 174493;
Best Local Similarity 87.5%; Pred. No. 4.9e-25;
Matches 266; Conservative 0; Mismatches 36; Indels 2; Gaps 1;

QY 673 TCTTGGCGGGCAGCGTGGCTCACACCTATATATCCAGCACCTTTGGGAGTCCAGCGGG 732
Db 119476 TATGGGCTGGGCACAGTGGCTCACACCTGTATATCCAGCACCTTTGGGAGCGGCGAGCAGG 119417

QY 733 CGGGTCACGAGGTCAAGAGATGGAGACCATCATGGCCAAACATGGTGAAACCCCTGTCTCTA 792
Db 119416 CGGATCACAAGGTCAAGAGATCGAGACCACCCCTGGCCACACATGGTGAAACCCCGTCTTTA 119357

QY 793 CTATAAATCAAAAAATTTATCTGGGTGTGGTGGCACATGCCTGTAATCCCAACTACTAG 852
Db 119356 CTAAAAATAC--AAAAATTAGCTGGGCATGGTGGTGCATGGCTGTAGTCCAGCTACTCG 119299

QY 853 GGAGGCTGAGGCAGGAGAATCGTTGAACCTGGGAGGCGGAGGTTCAGTGGAGCGGAGAT 912
Db 119298 GGAGGCTGAGGCAGGAGAATCTTGAACCCGGGAGGAGAGGTTGCAGTGGAGCTGAGAT 119239

QY 913 CGCACCATTTGCACCTCCAGCTGGCAACAGAGCGAGACTCCATCCCAAAAAACAAAAAC 972
Db 119238 CACACCACCTGCACCTCCAGCTGGCAACAGAGCGGAGACTCCTTCTAAAAAANAANA 119179

QY 973 AAAA 976
Db 119178 AAAA 119175

RESULT 12
US-09-764-877-2311
; Sequence 2311, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2311
; LENGTH: 7927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2311

Query Match      4.0%; Score 231.6; DB 10; Length 7927;
Best Local Similarity 85.7%; Pred. No. 4.8e-25;
Matches 269; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 664 AAAATCACTCTTGGCGGCGAGGTGGCTCACACCTATATATCCAGCACCTTTGGGAGTC 723
Db 3019 AAAATAAATGGTTGGCGGCGGCTCACACCTGTATATCCAGCATTTTGGGAGGC 3078

QY 724 CCAGGCGGCGGCTCACAGAGTCAAGAGATGGAGACCATCATGGCCAAACATGGTGAAAC 783
```

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Db 3079 CAAGCAGGTGGATCAGCAGGTGAGGAGTGCAGACCATCTGGCTAACACAGTGAACCC 3138
QY 784 CNGTCTCTACTATAATACAAAAAATTATCTGGGTGTGGTGGCACATGCCCTGTAAATCCC 843
Db 3139 CGGTCTCTACTAAAAATACAAAAAATTAGTGGCGTGGTGGCAGAGTGCCTGTAGTCCC 3198
QY 844 AACTACTAGGAGGCTGAGGCAGGAGATCGCTTGAACCTGGGAGCGGAGGTTGCAGTG 903
Db 3199 AGCTACTGGGAGGCTGAGGCAGGAGATGGCTGAACCCGCGAGTGGAGCTTGCAGTG 3258
QY 904 AGCCGAGATCGCACCATTCGACTCCAGCCTGG-CAACAGAGCGAGATCCATCCCAAAAC 962
Db 3259 AGCCAAAGATCGCGCCACTGCATCTCCAGCCTGGACAACAGAGCGAGACTCCATCTCAAAA 3318
QY 963 AAAACAAAACAAA 976
Db 3319 GAAAAAIAAAAAA 3332

RESULT 13
US-09-764-877-3785
; Sequence 3785, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3785
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3785

Query Match 4.0%; Score 231.4; DB 10; Length 337;
Best Local Similarity 85.2%; Pred. No. 3.8e-25;
Matches 270; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 673 TCTTGGCCGGGCAGCGTGGCTCACACCTATAATCCAGCACATTTGGGAGTCCCGAGCGGG 732
Db 9 TATAGCCGGCGTGTGGCTCACCGCTGTAATCCAGCACATTCGGGAGCGCGAGCGGG 68
QY 733 CGGGTCACGAGTCAAGAGATGGAGACCATCATGCCACATGGTGAACCCCTGTCTCTA 792
Db 69 CGGATCACGAGTCAAGAGATCGAGACCATCTGGCTAACACGGGTGAACCCCGTCTCTA 128
QY 793 CTATAAATCAAAAAAATTATCTGGGTGTGGTGGCACATGCTGTAAATCCCAACTACTAG 852
Db 129 CTGAAATACAAAAAATTAGCCGGCGTGTGGTGGCGGCGCTGTAGTCCAGCTACTTG 188
QY 853 GGAGGCTGAGGCAGGAGATCGCTTGAACCTGGGAGCGGAGGTTGCAGTGAAGCGGAGAT 912
Db 189 GGAGGCTGAGGCAGGAGATGGCGTGAACCCGGGAGCGGAGCTTGCAGTGAAGCGGAGAT 248
QY 913 CGCACCATTCGACTCCAGCCT-GGCACAGAGCGAGACTCCATCCCAAAACAAAACAAA 971
Db 249 CGCGCCACTGCATCTCAGCCTGGGCGACAGCGGAGACTCCGCTCTCAAAAAIAAAAAA 308
QY 972 CAAACCATGTAAACA 988
Db 309 AAAAAAIAAAAAA 325

RESULT 14
US-09-764-847-1173/c
; Sequence 1173, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1173
; LENGTH: 7683
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1173

Query Match 4.0%; Score 230.8; DB 10; Length 7683;
Best Local Similarity 83.5%; Pred. No. 6.2e-25;
Matches 274; Conservative 0; Mismatches 52; Indels 2; Gaps 1;

QY 649 TTAAAAATTCATTGTAATAAATCAGTCTTGGCCGGGCACGGTGGCTCACACCTATATATCCC 708
Db 7479 TTCATATCTTTTATAAAATTTTATTTCTTGGCTGGCAGGCTGCTCTGTAATCCC 7420
QY 709 AGCACTTTGGGAGTCCCGAGCGGCGGTCCAGAGTCAAGAGATCGAGACCATCATGCG 768
Db 7419 AGCACTTTGGGAGGCTGAGCGCGGCGATCACGAGGTGAGGATCGAGACCATCTGCG 7360
QY 769 CAACATGGTGAACCCCTCTCTACTATAAATACAAAAAATTTATCTGGGTGTGGTGGCA 828
Db 7359 CAACATGGTGAACCCCTCTCTACTATAAATAC--AAAAATTTGCTGGGCGTGGTGG 7302
QY 829 CATGCCGTGAATCCCAACTACTAGGAGGCTGAGGAGGAGTCCGTTGAACCTGGGAG 888
Db 7301 CGTGCCTGTAGTCCCGCTACTTTGGGAGGCTGAGGAGGAGTCCGTTGAACCGAGGAG 7242
QY 889 GCGGAGGTTCAGTGAAGCGGAGATCGCACCATTTGCATCCAGCTGGCAACAGAGCGAGA 948
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QY 949 CTCATCCCAACAAACAAACAAACAAA 976
Db 7181 CTCATCTCAAAAAAIAAAAAIAAAAAA 7154

RESULT 15
US-09-764-877-3325/c
; Sequence 3325, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3325
; LENGTH: 3813
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3325

Query Match 4.0%; Score 230.6; DB 10; Length 3813;
Best Local Similarity 83.3%; Pred. No. 6.2e-25;
Matches 274; Conservative 0; Mismatches 54; Indels 1; Gaps 1;

QY 674 CTTGGCCGGGCAGGCTGGCTCACACCTATAATCCACACATTTGGGAGTCCCGAGCGGG 733
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QY 734 GGGTCACGAGGTCAAGAGATGGAGACCATCATGGCCAAACATGGTGAACCCCTGTCTCTAC 793
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Qy 794 TATAAATACAAAAAATTATCTGGGTGTGGTGGCACATGCTGTAAATCCCAACTACTAGG 853
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Qy 854 GAGGCTGAGGCGAGGAGATCGCTTGAACCTGGGAGGCGGAGGTTGCAAGTGAGCCGAGATC 913
Db 3633 GAGGCTGAGGCGAGGAGATGCGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAACCAAGATC 3574
Qy 914 GCACCATTTGCACCTCCAGCCT-GGCAACAGAGCGAGACTCCATCCCAAAACAAACAAAC 972
Db 3573 GCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAATAAAAAA 3514
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Search completed: December 8, 2002, 21:58:35
Job time : 1768 secs

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BASE COUNT	317 a	190 c	300 g	223 t	4 others
ORIGIN					
Query Match	14.0%; Score 808.2; DB 9; Length 1034;				
Best Local Similarity	90.1%; Pred. No. 3e-91;				
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Db	121	ACTCGAAGCCCTCAGATGAATTTGAAGAACTGGAATCTTAAGTAAATCAACGTAGG	180		
QY	4611	CCTCACTCAATCTCAGACTTACCAAGTTA---AAGTTGAGAAGCTTGAACCTA	4662		
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QY	4663	----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCT	4718		
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QY	4839	AAACGTGTTCAAGCTTCTCTCAACTCACATATCTCAGACGCTTACTGGGACCAAA	4898		
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QY	4899	GGAGGCCCTTACTCAGATATTAGGACCACCTGGAGGGCCTGGATGACGAGGAGGAGG	4958		
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QY	4959	TGAGCATGAGGAGGATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGA	5018		
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QY	5019	GGAGGAGGAGGAGGTGAAGAGGAGGACGTGAGTCGAGGGGACGAGGAGATGAAGAGG	5078		
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QY	5079	TTATAACGATGAGGAGGTAGTGGGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAG	5138		
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QY	5139	GGTCAAGAGCGAAATGAGACCTGAGATGAGGAGGAAGATGATGACTAAGTAGAATA	5198		
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QY	5253	CCCCCTCAATCCTGCCCTGAAACTTACTTTTCTGATTGTAACTATGCTGTGGAA	5312		
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Db	901	CGAGAGGGGAAGTGTACTGGGGTGTGGAGGAGGAGGATGCGGGTGGGGTGGAAAT-	959		
QY	5373	AAATACTATTTTACTGCCAAATAAATAATATTTGTAATAATTAACATGGG	5423		
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DEFINITION	AL560249 LTI_FL011_BC1 Homo sapiens cDNA clone CS0DG002Y123 5 prime mRNA sequence.				
ACCESSION	AL560249				
VERSION	AL560249.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.				
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	/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"				
BASE COUNT	299 a	163 c	279 g	175 t	7 others
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Query Match	13.3%; Score 770; DB 9; Length 923;				
Best Local Similarity	92.1%; Pred. No. 1.7e-86;				
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QY	4447	CGAGATGAGGATGGCGCAGACGGATTTCATTACAGCTCGCGAACAGCGCCCTCTGAT	4506		
Db	121	CGAGATGAGGATGGCGCAGACGGATTTCATTACAGCTCGCGAACAGCGCCCTCTGAT	180		
QY	4507	GTGAAGAACTTGCCTCGGACACAGTCGGTCAATGAAGCAACTCGAAGCCCTCACA	4566		

Db	181	GTAAAGAACTTGCTCTGGACACAGTCGGTCAATGAAGCAAACTCGAAGGCCTCACA	240
Qy	4567	GATGAATTTGAAGAACTTGAATTCCTTAAGTAATAATCAACGAGCCCTCACCTCAATCTCA	4626
Db	241	GATGAATTTGAAGAACTTGAATTCCTTAAGTAATAATCAACGAGCCCTCACCTCAATCTCA	300
Qy	4627	GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG	4674
Db	301	AACCTTACCAAGTTAATAACAACTTAAGAAAGCTTGAACCTAAGCGGATAACAGAGCTCAGGG	360
Qy	4675	GGCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAAC	4734
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Qy	4735	AAAATTAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTA	4794
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Db	661	TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGG	720
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Db	721	GAAGAGGAGCCTGCTGAGGGGAGGAGGAGGAGGAGTGAAGAAGTTATAACGATGAGAG	780
Qy	5095	GTAGATGGCAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTCAAGAGCGAAA	5154
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Qy	5155	TGAAACCTGAAGATGAGGAGAGATGATGACTAGTGAATTAACCTATTTTGAAGAAAT	5214
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prime, mRNA sequence.			
ACCESSION			
AL533191			
VERSION			
AL533191.1 GI:12796684			
KEYWORDS			
EST.			
SOURCE			
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ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 894)			
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
JOURNAL			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
BP 191 91006 EVRY cedex - France			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.			
Location/Oualifiers			
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source			

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BASE COUNT 293 a 159 c 270 g 170 t 2 others
ORIGIN

Query Match 13.1%; Score 756.6; DB 9; Length 894;
Best Local Similarity 92.8%; Pred. No. 8e-85; 50; Indels 13; Gaps 3;
Matches 829; Conservative 1; Mismatches 50;
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QY 4655 TTGAACCTA-----AGAGTCTCAGGGGGCTCGAAGTATTGGCAAAAAGTCTCCAA 4705
Db 301 TTGAACCTA-----AGAGTCTCAGGGGGCTCGAAGTATTGGCAAAAAGTCTCCGA 360
QY 4706 ACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGACCTCAGCAATAGAGCCAC 4765
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QY 4765 TGAACAGTTAGAAACCTCAAGAGCTTAGACCTTTCAATTCGAGGTAAACCA-ACCTG 4824
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QY 4825 AACGACTACGGAGAAAACGTTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 4884
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QY 4885 TACTGGACCAAGAGAGGCCCTTTACTCAGATATTAGGACCACTGGAGGGCCTGGAT 4944
Db 541 GACCGGACCAAGAGAGGCCCTTACTCAGATATTAGGACCACTGGAGGGCCTGGAT 600
QY 4945 GACGAGGAGAGGTGACGATGAGGAGAGTATGATGAAGATGCTCAGTAGTGAAGAT 5004
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QY 5005 GAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5064
Db 661 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 5065 GAGGATGAAGAGGTTATTAACGATGAGAGGTAGATGGCGAGGAAGATCAAGAGAGCTT 5124

Db 721 GAGGTGAAGAGGTTATACCATGAGAGGTAGATGACGAGGAGATGAAGAAGACTT 780
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Db 781 GGTGAAGAGAAAGGGTCAGAAGCGAAACGAGAACCTGAAGATGAGGAGAGATGAT 840
QY 5185 GACTAAGTAGATACCTATTGTTGAAAAATCCCTATTGTTGACTGTTT 5237
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DEFINITION prime, mRNA sequence.
ACCESSION AL535686
VERSION AL535686.1 GI:12799179
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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BASE COUNT 291 a 156 c 267 g 160 t 1 others

Query Match 13.0%; Score 751; DB 9; Length 875;
Best Local Similarity 92.9%; Pred. No. 4e-84;
Matches 813; Conservative 0; Mismatches 50; Indels 12; Gaps 2;

QY 4358 AGCTTCAAGTCCGAAACGTCGGCCCTGCGTTCGAGGTTTATTGATTGATTCGGCT 4417
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QY 4418 GGCACGAGACCTCTCTGACAGACGAGCGGAGATGGAGATGGCGACGATTCATT 4477
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QY 4478 CAGAGCTGGGAACAGGGGCCCTCTGATGTGAAGAAGTTCCTCTGACACACATCGGT 4537
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 903)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/clone="CS0DE004YL15"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
/note="Organ: Placenta; Vector: pCMVSPORT 6; 1st strand

cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 298 a 160 c 271 g 164 t 10 others
ORIGIN

Query Match 12.8%; Score 741.8; DB 9; Length 903;
Best Local Similarity 91.7%; Pred. No. 5.4e-83;
Matches 821; Conservative 9; Mismatches 51; Indels 14; Gaps 4;

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QY 4336 GAGAACCGAGCGAGCTGGTTGAGTCTTCAAAGTCCTAAACAGTGGCGCGTGGTTTCGA 4395
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Db 1 GARAACCGAGCGGA-CTGTTTGAAGCTTCAAAGTCTTAAACCGCGCGCGTGGTTTCGG 59
QY 4396 GGTATTATTGATTTCGGCTGCGCAGCAGAGCCCTCTGCACACAGAGCGCGAGATG 4455
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Db 60 GTTTATTGATTGAATTCGCGCGCGGGAGCCCTCTGCARAGAGAGCGCGARAAWG 119
QY 4456 GAGATGGCAGACGAGTTCATTACAGACTGCGGAACAGCGGCCCTCTGTATGTCAAAGAA 4515
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Db 120 GAGAWGGCAGACGATTTCATTAGAGCTGCGGAACAGAGAGCCCTCTGTATGTGAARAA 179
QY 4516 CTGTCCTGGACACAGTCGCTGGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTT 4575
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 CTGTCTCTGGACACAGTCGCTGGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTT 239
QY 4576 GAAGAACTGGAATCTTAAGTAAATCAACGAGAGCCCTCACCTCAATCTCAGACTTACCA 4635
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Db 240 GAAGAACTGGAATCTTAAGTAAATCAACGAGAGCCCTCACCTCAATCTCAGACTTACCA 299
QY 4636 AAGTTA---AAGTTGAGAAAGCTTTGAAGT-----AGAGTCTCAGGGGCGCTGAA 4683
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Db 300 AAGTWAACAACTTAAGAACTTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 359
QY 4684 GTATTGGCAGAAAGTGTCCAAACCTCACGCATCTATATTAAAGTGCAACAAATTTAA 4743
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Db 360 GTATTGGCAGAAAGTGTCCAAACCTCACGCATCTAAATTTAAGTGCAACAAATTTAA 419
QY 4744 GACCTCAGCACAAATAGAGCCACTCAACAGTTAGAAACCTCAGAGCTTAGACCTTTTC 4803
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Db 420 GACCTCAGCACAAATAGAGCCACTGAAAAATTTAGAAACCTCAGAGCTTAGACCTTTTC 479
QY 4804 AATTGGAGGTAAACCACTGAACGACTACGAGAAACCGTGTCAAGCTTCTCCTCGAA 4863
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 480 AATTGGAGGTAAACCACTGAACGACTACCGAGAAATGCTGTCAAGCTTCTCCTCGCA 539
QY 4864 CTCATATCTCGACAGCTGTTACTGGGACCAAGAGGCGCCCTTACTCAGATATTGAG 4923
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Db 540 CTCATATCTCGACGCTATACCGGGGACGAAAGGAGGCGCCCTACTCGGATGCTGAG 599
QY 4924 GACCAGCTGGAGGCGCTGGATGACGAGAGGAGGCTGAGCATGAGGAGGATGATGAA 4983
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Db 600 GCCTACGTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGATGATGAA 659
QY 4984 GATGCTCAGGTAGTGGAGAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5043
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Db 660 GATGCTCAGGTAGTGGAGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAG 719
QY 5044 GACGTGAGTGGAGGCGGAGGAGGAGTGAAGAAGTTTATAACGATGAGAGGTTAGATGGC 5103
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 720 GACGTGAGTGGAGAGGAGGAGGAGTGAAGAAGTTTATAACGATGAGAGGTTAGATGAC 779
QY 5104 GAGGAAGTGAAGAAGCTTGG-TGAGAGAAAGGGGTTCAGAGCGAAATGAGAAC 5162
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Db 780 GAGGAAGTGAAGAAGCTTGGTTGAAGAAGAAAGGGGTTCAGAGCGAAATGAGAAC 839
QY 5163 TGAAGATCAGGAGAGATGATGACTAAGTAGAATAACCTTATTTTGAAAAATTC 5217
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Db 840 TGAAGATGAGGAGAGATGATGACTAAGTCGAATAACCTATTTTGAATAATTCY 894

RESULT 6
AL537874
LOCUS AL537874
DEFINITION AL537874 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF028YN19 5
prime, mRNA sequence.
ACCESSION AL537874
VERSION AL537874
KEYWORDS AL537874.1 GI:12801367
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
location/Qualifiers
1..870
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 290 a 156 c 265 g 155 t 4 others
ORIGIN

Query Match 12.7%; Score 735; DB 9; Length 870;
Best Local Similarity 91.9%; Pred. No. 3.8e-82;
Matches 797; Conservative 4; Mismatches 54; Indels 12; Gaps 2;

QY 4358 AGCTTTCAAAGTCTTAAACAGTGGCGCGTTCGAGTTTATGATTGAATTCGGCT 4417
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Db 1 ARCTTTCAAARTCCWAAACAGCGCGCGTGGGTTTCGGGTTTATGATTGAATTCGGCC 60
QY 4418 GGCACGAGAGCCCTCTGCACACAGAGAGCGGAGATGAGATGGCAGACGATTCATT 4477
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Db 61 GCGCGGGAGCCCTCTGCAGAGAGAGAGCGGAGATGAGATGGCAGACGATTCATT 120
QY 4478 CAGAGCTCGGAAACAGGGCGCCCTCTGATGTGAAGAACTTCGCCCTGGACACAGTCGCT 4537
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Db 121 TAGAGCTCGGRACAGAGCGCCCTCTGATGTGAAGAACTTGTCTCGACACAGTCGCT 180
QY 4538 CGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAAGTGAATTTAAAGTA 4597
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 CGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAAGTGAATTTAAAGTA 240
QY 4598 AATCAACGAGCCCTCACCTCAATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGC 4654
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 CAATCAACGTAGCCCTCACCTCAATCTGCAAACTTACCAAGTAAACAACTTAAGAAGC 300
QY 4655 TTGAAGTCA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCAA 4705
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 TTGAAGTCAAGGATACACAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCA 360
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Qy	4706	ACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGAGCTCAGCACATAGAGCCAC	4765
Db	361	ACCTCAGCATCTAATTTAAGTGGCAACAAATTAAGAGCTCAGCACATAGAGCCAC	420
Qy	4766	TGAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATTGGAGGTAAACCACTGA	4825
Db	421	TGAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATTGGAGGTAAACCACTGA	480
Qy	4826	AGCACTACGGAACAAACGTTTCAAGCTTCCTCGCACTCACATATCTCGACAGCTGTT	4885
Db	481	AGCACTACGGAACAAATGTTTCAAGCTTCCTCGCACTCACATATCTCGACGCTATG	540
Qy	4886	ACTGGACCCACAGAGGCCCCCTTACTCAGATATTAGGACACACCTGGAGGCGCTGGATG	4945
Db	541	ACCGGACACAGAGGCCCCCTGACTCGATGCTGAGGCTACGTGAGGCGCTGGATG	600
Qy	4946	ACGAGAGAGGGTGAGCTAGAGGAGGTATGATGAAGATGCTCAGGTAGTGAAGATG	5005
Db	601	ATGAGGAGGAGTGAAGTGAAGGAGGTATGATGAAGATGCTCAGGTAGTGAAGATG	660
Qy	5006	AGGAGGCCAGAGGAGGAGGAGGTGAAGAGGAGGAGCTGAGTGAAGGAGGAGG	5065
Db	661	AGGAGGAGGAGTGAAGGAGGAGGAGGTGAAGAGGAGGAGCTGAGTGAAGGAGGAGG	720
Qy	5066	AGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGGCGAGGAGATGAAGAAGCTTG	5125
Db	721	AGGATGAAGAAGTTATAACGATGGAGAGGTAGATGAAGAAGCTGAAGAAGCTTG	780
Qy	5126	GTGAAGAAGAGGGGTGAGAGCGAATAGAACCTTGAAGATGAGGAGAGATGATG	5185
Db	781	GTGAAGAAGAGGGGTGAGAGCGAATAGAACCTTGAAGATGAGGAGAGATGATG	840
Qy	5186	ACTAAGTGAATAACCTATTGTTGAAA 5212	
Db	841	ACTAAGTGAATAACCTATTGTTGAAA 867	
RESULT 7			
LOCUS	BM904155	1035 bp mRNA linear EST 12-MAR-2002	
DEFINITION	AGENCOURT_6692842 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5499610	5', mRNA sequence.	
ACCESSION	BM904155		
VERSION	BM904155.1	GI:19354489	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/		
TITLE	1 (bases 1 to 1035)		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Staud Email: cgabbs-remail.nih.gov Tissue Procurement: Lou Staud CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12133 row: d column: 11 High quality sequence stop: 674. Location/Qualifiers 1. .1035 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5499610" /clone_lib="NIH_MGC_85" /tissue_type="lymphoma, cell line" /lab_host="DH10B (phage-resistant)"		
FEATURES	source		

/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT	325 a	204 c	301 g	205 t
ORIGIN				
Query Match	12.7%	Score 732.6;	DB 14;	Length 1035;
Best Local Similarity	87.3%;	Pred. No. 7e-82;		
Matches	858;	Conservative	0;	Mismatches 99; Indels 26; Gaps 4;
Qy	4342	CGAGCGAGCTGGTGTAGTCTTCAAAGCTCTAAACGTCGCGCGCTGGTTCAGAGTTTA	4401	
Db	1	CGAGCGAGCTGGTGTAGCTTCAAAGCTCTAAACGTCGCGCGCTGGTTCGCGGTTTA	60	
Qy	4402	TTGATTCAATTCGCTGCGACAGAGCTCTGCAGACAGAGCGCGAGAGATGGAGATG	4461	
Db	61	TTGATTGAATTCGCGCGCGCGGAGCTCTGCAGAGAGAGCGCGAGAGATGGAGATG	120	
Qy	4462	GGCAGACGGATTCAATTCAGAGCTGCGGAACAGGCGGCCCTCTGATGTGAAGAACTTGGC	4521	
Db	121	GGCAGACGGATTCAATTCAGAGCTGCGGAACAGGACGCCCTCTGATGTGAAGAACTTGTG	180	
Qy	4522	CTGGAACAACAGTCGGTCCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAGAA	4581	
Db	181	CTGGAACAACAGTCGGTCCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAGAA	240	
Qy	4582	CTGGAATTCCTAAGTAAATCAACGGAGGCTCACCTCAATCTCAGACTTACCAAGTTA	4641	
Db	241	CTGGAATTCCTAAGTAAATCAACGGAGGCTCACCTCAATCTCAGACTTACCAAGTTA	300	
Qy	4642	---AAGTTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGGGCGCTGGAAGTATTG	4689	
Db	301	AACAACTTAAGAGCTTGAACCTAAGCGATAACAGAGCTCTCAGGGGCGCTGGAAGTATTG	360	
Qy	4690	GCAGAAAGTGTCCAAACCTCACGCATCTATATTAAGTGCAGCAACAAATTAAGACCTC	4749	
Db	361	GCAGAAAGTGTCCGAAACCTCACGCATCTGAATTTAAGTGCAGCAACAAATTAAGACCTC	420	
Qy	4750	AGCAATAGAGCCACCTGAACAGTGTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTGC	4809	
Db	421	AGCAATAGAGCCACCTGAACAGTGTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTGC	480	
Qy	4810	GAGTAACCAACCTGAACAGCTACGAGAGAAACCGTGTCAAGCTTCTCGCAACTCACA	4869	
Db	481	GAGTAACCAACCTGAACAGCTACGAGAGAAACCGTGTGTCAAGCTTCTCGCAACTCACA	540	
Qy	4870	TATCTGACAGCTGTTACTGGGACCAAGAGGCGCCCTTACTCAGATATGAGGACCA	4929	
Db	541	TATCTGACAGCTGTTACTGGGACCAAGAGGCGCCCTGACTCGGATGCTGAGGCGCTAC	600	
Qy	4930	GTGAGGCGCTGGATGACGAGGAGGCGGTGAGCATGAGGAGGATGATGATGAAGATGCT	4989	
Db	601	GTGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGATGATGATGAAGATGCT	660	
Qy	4990	CAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5049	
Db	661	CAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	720	
Qy	5050	AGTGAGGCGGAGGAGGAGGATGAAGAGGTTATACCATGAGGAGGATGATGAGGAGGAA	5109	
Db	721	AGTGAGGAGGAGGAGGAGGATGAAGAGGTTATACCATGAGGAGGATGATGAGGAGGAA	780	
Qy	5110	GATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCAGAGCGCAAAATGAGAACCTTGAAGAT	5169	
Db	781	GATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCAGAGCGCAAAATGAGAACCTTGAAGAT	840	
Qy	5170	GAGGAGAGAGATGATGACTAAGTAAATAACCTTATTTTGAAGAAATTCCTATTGTTG---	5224	
Db	841	GAGGAGAGAGATGATGACTAAGGAGGAAATACCTTATTTTGAAGAAATTCCTATTGTTG	900	
Qy	5225	-----ATTGACTGTTTTTACCCTATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	5275	

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Db 901 TTGACGGGTTTAAACCATATCCCTTTCCGCCCTTCAATTCCTGGCGCCTG 960
QY 5276 AACCTACTTTTTCTGATTGTAA 5298
Db 961 AAAACTTATTTTTTCCCGGAA 983

RESULT 8
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LOCUS AL547157 LTI_NFL006_PL2 875 bp mRNA linear EST 27-FEB-2001
DEFINITION AL547157 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1010YL13 5
prime, mRNA sequence.
ACCESSION AL547157
VERSION AL547157.1 GI:12880969
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/organism="Homo sapiens"
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/clone="CS0D1010YL13"
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 288 a 157 c 267 g 161 t 2 others
ORIGIN

Query Match 12.6%; Score 731.6; DB 9; Length 875;
Best Local Similarity 92.4%; Pred. No. 1e-81;
Matches 804; Conservative 2; Mismatches 51; Indels 13; Gaps 3;

QY 4359 GTCTTCAAAGTCCTAAACGTGGCGCGTGGTTCGAGGTTTATTGATTCGAATTCGGCTG 4418
Db 1 GCCTTCAAAGTCCTAAACGCGCGCGTGGTTCGAGGTTTATTGATTCGAATTCGGCGG 60
QY 4419 GCACGAGGCTCTGCACAGAGAGCGAGAGATGGAGATGGGACGCGGATTCATTC 4478
Db 61 GCGCGGAGGCTCTGCACAGAGAGAGCGCGAGATGGAGATGGGACGCGGATTCATTT 120
QY 4479 AGAGCTCGGGAACAGGCGCGCTCTGATGTGAAGAACTTGCCTTGGACAACAGTCGGTC 4538
Db 121 AGAGCTCGGGAACAGGAGCGCCTCTGATGTGAAGAACTTGTCTCGACAACAGTCGGTC 180
QY 4539 GAATGAAGGCAAACTCAAGCCCTCAGATGAATTTGAAGAACTGGAATTCITAGTAA 4598
Db 181 GAATGAAGGCAAACTCAAGGCGCTCAGATGAATTTGAAGAACTGGAATTCITAGTAC 240
QY 4599 AATCAACGGAGGCGCTCACTCAATCTCAGACTTACCAAGCTTA---AAGTTGAGAAGCT 4655
Db 241 AATCAACGAGGCGCTCACTCAATCTCAGACTTACCAAGCTTAACCAAACTTAAAGAGCT 300
QY 4656 TGAACATA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCAAA 4706
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Db 301 TGAACCTAAGCGATAACAGAGTCTCAGGGCGCTGGAGTATTGGCAGAAAAGTGTCCGAA 360
QY 4707 CCTCAGCATCTATATTTAAGTGGCAACAAAATTAAGACCTCAGCACAAATAGACCACT 4766
Db 361 CCTCAGCATCTAAATTTAAGTGGCAACAAAATTAAGACCTCAGCACAAATAGACCACT 420
QY 4767 GAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTGGGAGGTAAACCAACTGAA 4826
Db 421 GAAAAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTGGGAGGTAAACCAACTGAA 480
QY 4827 CGACTACGGGAAAACGCTGTTCAAGCTTCTCTGCAAACTCACATATCTCGACAGCTGTTA 4886
Db 481 CGACTACCGGAAAATGTCTTCAAGCTCTCCCGCAACTCACATATCTCGACGGGTATCA 540
QY 4887 CTGGGACCACAAGAGGGCCCCCTTACTCAGATATTGAGGACCACGCTGGAGGGCTGGATGA 4946
Db 541 CCGGGACGACAAGGAGGCGCCCTGACTCGGATGCTGAGGGCTACGTTGGAGGGCTGGATGA 600
QY 4947 CGAGGAGGAGGGTGTGACATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGA 5006
Db 601 TGAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGA 660
QY 5007 GGAGGCGGAGGAGGAGGAGGAGGAGTGAAGTGAAGGAGGAGCTGAGTGGAGGGACGAGGA 5066
Db 661 GGAGGACGAGGATGAGGAGGAGGAGGAGTGAAGTGAAGGAGGAGCTGAGTGGAGAGGAGGA 720
QY 5067 GGATGAAGAAGGTTATACGATGGAGAGTAGATGCGGAGGAAGATGAAGAAGAGCTTTGG 5126
Db 721 GGATGAAGAAGGTTATACGATGGAGAGCTAGTAGACGAGGAAGATGAAGAAGAGCTTTGG 780
QY 5127 TGAAGAAGAAGGGGTTCAGAACGCGAAAATGAGAACCTGAAGATGAGGAGAGAGATGATGA 5186
Db 781 TGAAGAAGAAGGGGTTCAGAACGCGAAAACGAGAACTGAAGATGAGGAGGAAGATGATGA 840
QY 5187 CTAAGTGAAGATAACCTATTATTTGAAAAAATTC 5216
Db 841 CTAAGT-GGATACCTATTATTTGAAAAATTC 869

RESULT 9
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LOCUS AL571434 LTI_NFL006_PL2 894 bp mRNA linear EST 16-FEB-2001
DEFINITION AL571434 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1023YE09 3
prime, mRNA sequence.
ACCESSION AL571434
VERSION AL571434.1 GI:12928726
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 894)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. .894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1023YE09"
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
```



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Db 421 TAGAGCMAGTGAAGAAAGTTAGAAAACCTCAAGAGCTTAGAACCTTTTCAATTGCGAGGTAA 480
QY 4817 CCAACCTGAACGACTACGAGAAACAGTGTTCAGAGCTTCCTCGCAACTCACATATCTCG 4876
Db 481 CCAACCTGAACGACTACGAGAAATGTGTTCAAGTCTCTCCGCAACTCACATATCTCG 540
QY 4877 ACAGCTGTACTGGGACACAAAGAGGCCCTTACTCAGATATTGAGGACCACGCTGGAGG 4936
Db 541 ACGGCTATGACCGGACGACAAAGAGGCCCTGACTCGGATGCTGAGGGCTACGCTGGAGG 600
QY 4937 GCCTGGATGACGAGAGAGGGTGCAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAG 4996
Db 601 GCCTGGATGATGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAG 660
QY 4997 TGGAGATGAGGAGGCGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5056
Db 661 TGGAGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 5057 GGGACGAGGAGGATGAAGAAGGTTTAAACGATGAGAGGTAGATGAGGAGGAGGAGGAGG 5116
Db 721 AGGAGGAGGAGGATGAAGAAGGTTTAAACGATGAGAGGTAGATGAGGAGGAGGAGGAGG 780
QY 5117 AAGAGCTTGGTGAAGAAAGAGGGTGCAGAAAGCGAAATCAGAACCTGAAGATGAGGAG 5176
Db 781 AAGAGCTTGGTGAAGAAAGAGGGTGCAGAAAGCGAAATCAGAACCTGAAGATGAGGAGG 840
QY 5177 AAGATGATGACTAAGT 5192
Db 841 -AGATGATGACTAAGT 855

RESULT 11
LOCUS AL517375 992 bp mRNA linear EST 13-FEB-2001
DEFINITION AL517375 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA003YC02 5
prime, mRNA sequence.
ACCESSION AL517375
VERSION AL517375.1 GI:12780868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
301 a 174 c 289 g 217 t 11 others
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BASE COUNT
ORIGIN

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Query Match 12.3%; Score 710.4; DB 9; Length 992;
Best Local Similarity 88.4%; Pred. No. 4e-79;
Matches 813; Conservative 8; Mismatches 81; Indels 18; Gaps 4;

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QY 4515 ACTTTCCTCGGACCAACAGTCGGTCGAATGAAGCAAACTCGAAGCCCTCACAGATGAATT 4574
Db 61 ACTTTCCTCGGACCAACAGTCGGTCGAATGAAGCAAACTCGAAGCCCTCACAGATGAATT 120
QY 4575 TGAAGAACTGGAAATCTTAAAGTAAATAACAACGAGGCCCTCACCTCAATCTCAGACTTACC 4634
Db 121 TGAAGAACTGGAAATCTTAAAGTAAATAACAACGAGGCCCTCACCTCAATCGCAAACTTACC 180
QY 4635 AAAGTTA---AAGTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGGGCCCTGGA 4682
Db 181 AAAGTTA---AAGTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGGGCCCTGGA 240
QY 4683 AGTATTGGCAGAAAAGTGTCCTCAAACTCAGGCATCTATATTTAAAGTGGCAACAAAATTA 4742
Db 241 AGTATTGGCAGAAAAGTGTCCTCAAACTCAGGCATCTAATTTAAAGTGGCAACAAAATTA 300
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QY 4863 ACTCACATATCTCGACAGCTGTTTACTGGACCACACAGGAGGCCCTTACTTCAGATATTGA 4922
Db 421 ACTCACATATCTCGACAGCTGTTTACTGGACCACACAGGAGGCCCTGACTCGGATCTGA 480
QY 4923 GGACACAGTGGAGGGCCCTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4982
Db 481 GGGCTACGTGGAGGGCCCTGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 4983 AGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5042
Db 541 AGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 5043 GGACGTGACTGGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGG 5102
Db 601 GGACGTGACTGGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGA 660
QY 5103 CGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAATGAGAAC 5162
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QY 5223 TGATTGACTGTTTTTACCCATATATCCCTCCCCCTC---CAATCCTGCCCCCTGAAACT 5279
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QY 5280 TACTTTTTTCTCATGTACATCTGCTGGGAATCAGACGGGAAAGATGTACTGGGGGTT 5339
Db 841 TATTTTTTTCTCATGTAGAGTGTCTGGGACGAGA---GGGGAGAGTGTCTCTGGGGGTC 897
QY 5340 GTGAGGAGGAGGAGGAGGAGGAGG 5359
Db 898 GGGGGGGGTGCGGGGTGGG 917

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AK020753
LOCUS AK020753 1141 bp mRNA linear HTC 19-JAN-2002
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QY 4682 AAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTA 4741
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QY 4802 TCAATTCGAGGTAACCAACTCAAGCACTACGAGAAACGTTCAAGCTT-CTCCTG 4860
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QY 4861 CAATCACAATATCTCGACAGCTGTTACTGGGACCAAGAGGCCCTTACTCAGATATT 4920
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QY 4921 GAGGACCACTGGAGGCCCTGGATGAGGAGGAGGAGGAGGATGAGGAGGAGTATGAT 4980
Db 602 AAGGGCTACCTGGA-----GGATGACGACGAGGAGAGATGAGGATAAGGAGGAGTATGAT 655
QY 4981 GAAGATGCTCAGGTAGTGGAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
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QY 5041 GAGGACGTGAGTGGAGGAGGAGGAGGAGTGAAGAAGGTTATACGATGAGGAGGATGAT 5100
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DEFINITION BQ232856 895 bp mRNA linear EST 02-MAY-2002
AGENCOURT_7567365 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5060491
5', mRNA sequence.
ACCESSION BQ232856
VERSION BQ232856.1 GI:20414256
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-re@mail.nih.gov
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Tissue Procurement: DCTD/DTP/Cazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL3328 row: n column: 12
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Average insert size 1.8 kb. Library constructed by Life
Technologies."

BASE COUNT 294 a 163 c 276 g 161 t 1 others
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Query Match 12.1%; Score 702.8; DB 14; Length 895;
Best Local Similarity 92.2%; Pred. No. 3.7e-78;
Matches 799; Conservative 0; Mismatches 53; Indels 15; Gaps 5;

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QY 4871 ATCTCGACAGCTGTTACTGGGACCAACAAGGAGGCCCTTACTCAGATATTAGGACCACG 4930
Db 541 ATCTCGAGGCTATGACCGGAGCAACAAGGAGGCCCTGACTCGGATGCTGAGGCTACG 600
QY 4931 TGGAGGCGCTCGATCAGCAGGAGGAGGAGGATGAGCATGAGGAGGAGTATGATGAAGTCTC 4990
Db 601 TGGAGGCGCTCGATGATGAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGTCTC 660
QY 4991 AGGTAGTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5050

||||| 661 AGGTAGTGAAGACGAGGAGGAGGATGANGAGGAGGAGGAGTGAACAGGAGGAGCTGA 720
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VERSION AL545880.1 GI:12878473
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 834)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 272 a 153 c 257 g 148 t 4 others
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Query Match 12.1%; Score 699.4; DB 9; Length 834;
Best Local Similarity 92.2%; Pred. No. 1e-77;
Matches 759; Conservative 3; Mismatches 49; Indels 12; Gaps 2;

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QY 4471 ATTCATTTCAGAGCTCGGGAACAGGCGCCCTCTGATGTGAAGAAGTTCGCCCGACAAC 4530
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Db 188 AGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTC 247
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QY 4648 AGAAGCTTTGAATA-----AGAGTCTCAGGGGGCTGGAAGTATTTGGCAGAAAAG 4698
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QY 4819 AACCTGAACGACTACGGAGAAACGTTTCAAGCTTCTCCGCAACTCACATATCTCGAC 4878
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QY 4879 AGCTGTACTGGACACAAAGAGGCGCCCTTACTCAGATATTGAGGACCACCTGAGGGC 4938
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Db 788 GAGCTGGTGAAGAAGAAAGGGTTCAGAAAGCGAAACGAGAAAC 830

RESULT 15
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DEFINITION prime, mRNA sequence.
ACCESSION AL518247
VERSION AL518247.1 GI:12781740
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 802)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer.. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 258 a 148 c 248 g 143 t 5 others
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Query Match 11.6%; Score 673.2; DB 9; Length 802;
Best Local Similarity 91.8%; Pred.No.1.8e-74;
Matches 735; Conservative 2; Mismatches 52; Indels 12; Gaps 2;

QY 4353 GGTGAGTCTTCAAAGTCTTAAACGTGCGCGCGTGGGTTTCGAGGTTTATTGATTGAATT 4412
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QY 4413 CGGCTGCCAGAGAGCCTCTCCAGACAGAGAGCGGAGAGATGGAGTGGCGACACGGAT 4472
Db 62 CCGCGCGCGCGGAGCGCTCTCCAGAGAGAGAGCGGAGAVAMGAGACGGCGACACGGAT 121

QY 4473 TCATTACAGAGTCGGGAACAGGGCGCCCTCTGATGTGAAGAACTTCCCTCGACAAACAG 4532
Db 122 TCATTAGAGCTGGGNAACAGAGCGCCCTCTGATGTGAAGAACTTGTCTCGACAAACAG 181

QY 4533 TCGGTGCAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATTCCT 4592
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QY 4593 AAGTAAATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAG 4649
Db 242 AAGTAAATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAG 301

QY 4650 AAAGCTTGAACTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGCGACAAAAGTG 4700
Db 302 GAAGCTTGAACTAAGCGATAACAGAGCTTCAGGGGCGCTGGAAGTATTGCGACAAAAGTG 361

QY 4701 TCCAAACCTCACCGATCTATATTTAAGTGGCAACAAAATTAAGACCTCAGCAACAATAGA 4760
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QY 4941 GGATGACGAGGAGGAGGTGAGCATGAGGAGGATGATGATGAGATGCTCAGGTAGTGA 5000
Db 602 GGATGATGAGGAGGAGGTGAGCATGAGGAGGATGATGATGAGATGCTCAGGTAGTGA 661

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Db 722 GGAGGAGGATGAAGAGGTTTAAAGCATGGAGAGTGAATGACGAGGAGATGACGAGGAGATGAAGAAGA 781

QY 5121 GCTTGTGAAGAAGAAAGGGG 5141
Db 782 RCTTGTGAGAGAAAGGGG 802

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Job time : 4922 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 14:59:43 ; Search time 7694 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues
Total number of hits satisfying chosen parameters: 49582208

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2441.2	42.2	3955	36	US-09-976-594-207
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6	925.6	16.0	1197	32	US-10-216-583-94
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23 917.6 15.9 2449 42 US-10-216-583-601 Sequence 601, App
24 889 15.4 889 22 US-09-591-500-3 Sequence 3, Appl
25 883 15.3 1155 1 PCT-US01-08631-12193 Sequence 12193, A
26 869.2 15.0 2398 16 US-09-205-070-14975 Sequence 14975, A
27 869.2 15.0 2398 17 US-09-340-623-14975 Sequence 14975, A
28 869.2 15.0 2398 33 US-09-898-888-14975 Sequence 14975, A
29 869.2 15.0 2398 33 US-09-898-888A-14975 Sequence 14975, A
30 867.8 15.0 1052 1 PCT-US02-25766-3866 Sequence 3866, Ap
31 866.6 15.0 895 22 US-09-591-500-15 Sequence 15, Appl
32 865 15.0 895 22 US-09-591-500-21 Sequence 21, Appl
33 839.4 14.5 895 22 US-09-591-500-23 Sequence 23, Appl
34 831.4 14.4 907 22 US-09-591-500-6 Sequence 6, Appl
35 791 13.7 916 14 US-09-038-847A-2 Sequence 2, Appl
36 791 13.7 916 17 US-09-393-302-25 Sequence 25, Appl
37 791 13.7 916 31 US-09-825-886-25 Sequence 25, Appl
38 764.4 13.2 925 37 US-09-997-722-245 Sequence 245, App
39 764.4 13.2 925 38 US-10-035-832-1497 Sequence 1497, App
40 762.6 13.2 907 22 US-09-591-500-13 Sequence 13, Appl
41 761 13.2 907 22 US-09-591-500-25 Sequence 25, Appl
42 760.2 13.1 906 22 US-09-591-500-33 Sequence 33, Appl
43 757.8 13.1 907 22 US-09-591-500-28 Sequence 28, Appl
44 753 13.0 907 22 US-09-591-500-9 Sequence 9, Appl
45 751.6 13.0 908 22 US-09-591-500-32 Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-591-500-1
; Sequence 1, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5785
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4453)..(5154)
; OTHER INFORMATION:
US-09-591-500-1

Query Match 100.0%; Score 5785; DB 22; Length 5785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5701 AATAATTTGCTAAAGCAAAATTTTGGAAAAATAATAATGCACTTTATACCTTGATTTATT 5760
QY 5761 TATTAAAACAATGATTTATAAGCTT 5785
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Db 5761 TATTAAACAAATGATTTATAAGCTT 5785

RESULT 2

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; Sequence 13384, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 p
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 13384
; LENGTH: 6753
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 419322.6
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 677-976, 1431-1454, 2474-2802, 5035, 5037, 5071
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-13384

Query Match 78.9%; Score 4563.6; DB 61; Length 6753;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 4688; Conservative 0; Mismatches 745; Indels 21; Gaps 5;

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QY 61 CTTTTTCTTATGTAACCTCTCATAAACACATAGCATATATGTTTGGCATGTTTTCTTCCCT 120
Db 61 CTTTTTCTTATGTAACCTCTCATAAACACATAGCATATATGTTTGGCATGTTTTCTTCCCT 120
QY 121 ATCAGTTGCAAGTTPCCAGCAGAGCTGATATATTTTCATTTTCATTCGCTACTATAGCCCTA 180
Db 121 ATCAGTTGCAAGTTPCCAGCAGAGCTGATATATTTTCATTTTCATTCGCTACTATAGCCCTA 180
QY 181 GAGCCTGACATAGTTTCTGGCTGTGAATGCTCAATAAATAATTTGTTAAATGAGTAGAAA 240
Db 181 GAGCCTGACATAGTTTCTGGCTGTGAATGCTCAATAAATAATTTGTTAAATGAGTAGAAA 240
QY 241 CATAAAGTATCTATTTTCATTTCAAGGAAGAATAATATAGCTACATTTTCTTTTCTTGCC 300
Db 241 CATAAAGTATCTATTTTCATTTCAAGGAAGAATAATATAGCTACATTTTCTTTTCTTGCC 300
QY 301 TTAATATTTGAGGAATTTGCTTATATGTCATATAAAAAAGTTTAAAGCCCTTATACATTAT 360
Db 301 TTAATATTTGAGGAATTTGCTTATATGTCATATAAAAAAGTTTAAAGCCCTTATACATTAT 360
QY 361 ACTAAGGAATTTGGACATTTAAATCAAGCTAGCGCTTTCTATAAACAATACTGAATTTTC 420
Db 361 ACTAAGGAATTTGGACATTTAAATCAAGCTAGCGCTTTCTATAAACAATACTGAATTTTC 420
QY 421 TGCCCTAAATTTGTTCCCTTCCCTATCTTCCCATTTGAGTGAACACCAAAATCCCTCTAG 480
|||||

Db 421 TGTCCTTAAATTTGTTCTTCCCTATCTTCCCATTTGAGATGACACCAAAATCCCTCTAG 480
QY 481 CTGCTCAAAACCAAGTACCCGATATGTTATCTTAATATCTTCTTACCTTGCCTTCTCATAT 540
Db 481 CTGCTCAAAACCAAGTACCCGATATGTTATCTTAATATCTTCTTACCTTGCCTTCTCATAT 540
QY 541 GCAATTTGTTAAACAAGTCATCTTCAGTCGTATCCATTTATCTCCCTTTCCAGACACCA 600
Db 541 GCAATTTGTTAAACAAGTCATCTTCAGTCGTATCCATTTATCTCCCTTTCCAGACACCA 600
QY 601 ACATGCTTGTGACTATATGCTACAATAGCTCCCAACTCTTGTCCCTACTTAAATTCATT 660
Db 601 ACATGCTTGTGACTATATGCTACAATAGCTCCCAACTCTTGTCCCTACTTAAATTCATT 660
QY 661 GTAAAAAATCAGTCTTTNN 720
Db 661 GTAAAAAATCAGTCTTTNN 720
QY 721 GTCCAGGGCGGGGTACAGGTCACAGATGAGAGACCATCATGCGCAACATGCGTAA 780
Db 721 NNN 780
QY 781 ACCCTGTCTCTACTATAATAACAAAAAATATCTGGTGTGGTGGCACATGCTGTAAT 840
Db 781 NNN 840
QY 841 CCCAACTACTAGGAGGCTGAGGACGAGAAATCGCTTGAACTGGGAGCGGAGGTGCA 900
Db 841 NNN 900
QY 901 GTGAGCCGAGATGCGACCATTCACCTCCAGCTGGCAACAGAGGAGACTCCATCCCAA 960
Db 901 NNN 960
QY 961 ACAAAAACAAAACCAACCATGCTGTAAAAACATGTGTAAAAACATGTCTGTTTCAG 1020
Db 961 NNN 1020
QY 1021 AAGTCTTACATGCTTTTTCATTTATGCTAAGATAAAACCAAAATGATTTCTTGGTTCT 1080
Db 1021 AAGTCTTACATGCTTTTTCATTTATGCTAAGATAAAACCAAAATGATTTCTTGGTTCT 1080
QY 1081 AAGCCCAACAAAATAAGAGTGTCTTCAGCAACCTGTGTTCTTCGCGCATGCTTTCCCT 1140
Db 1081 AAGCCCAACAAAATAAGAGTGTCTTCAGCAACCTGTGTTCTTCGCGCATGCTTTCCCT 1140
QY 1141 AGCTCACTCTTTTAGGCAAGTCGACCTGATTTTCTTCTGTAGTCTGTTTCTGCCTCG 1200
Db 1141 AGCTCACTCTTTTAGGCAAGTCGACCTGATTTTCTTCTGTAGTCTGTTTCTGCCTCG 1200
QY 1201 TGGTCTGGCTTTCTTCTGTTAGTCTGTTTCCACCTCGTGGTCTGGTCTGGCTCTTCA 1260
Db 1201 TGGTCTGGCTTTCTTCTGTTAGTCTGTTTCCACCTCGTGGTCTGGTCTGGCTCTTCA 1260
QY 1261 TTCTGCTGGAATGCTCTCCACTCCAGATCCTTACTAGATCTTAGCTCAGTCAATCACCT 1320
Db 1261 TTCTGCTGGAATGCTCTCCACTCCAGATCCTTACTAGATCTTAGCTCAGTCAATCACCT 1320
QY 1321 CGCAGAGATCTTCCAAACCATTCACCTGCATACACCTATGGCTGCTCCCTAGAGAAT 1380
Db 1321 CGCAGAGATCTTCCAAACCATTCACCTGCATACACCTATGGCTGCTCCCTAGAGAAT 1380
QY 1381 CATTCTGTTTCTTCTCCTCTAGCATTACTGCTTTCTGAAATTTATCTACTTTGATTTGT 1440
Db 1381 CATTCTGTTTCTTCTCCTCTAGCATTACTGCTTTCTGAAATTTATCTACTTTGATTTGT 1440
QY 1441 TTATTTCTTTCTTCTTCTTACTAGGATACCTGGGTGCTAATAAGGAGGATATTTCTCTC 1500
Db 1441 NNN 1500
QY 1501 TTATTTACTGTTTATAAATTAATGCTTAGGCTGTAGAAGTTATACAATTTTGAAGAATA 1560
Db 1501 TTATTTACTGTTTATAAATTAATGCTTAGGCTGTAGAAGTTATACAATTTTGAAGAATA 1560

Db 3721 CTCATTAATAAATGTTCTCAGAAAGTAAATAATATTCCTCTCTAAATAACATAC 3780
QY 3781 ATGCCACTCAAAATTTTATCTCTACACATTCGCGTATCTAAACCTAGTTAGATACTTTG 3840
Db 3781 ATGCCACTCAAAATTTTATCTCTACACATTCGCGTATCTAAACCTAGTTAGATACTTTG 3840
QY 3841 GTTTTAGTATAATCTGACAGAACAGATACAAACCAAGATACATTTGTGAGTCAGAACTGG 3900
Db 3841 GTTTTAGTATAATCTGACAGAACAGATACAAACCAAGATACATTTGTGAGTCAGAACTGG 3900
QY 3901 AAAATTCATAATCATGATGATACCAATAAAAGATAGATTTAGCTTTTACAGGATGTTT 3960
Db 3901 AAAATTCATAATCATGATGATACCAATAAAAGATAGATTTAGCTTTTACAGGATGTTT 3960
QY 3961 TTGGCATTTTATCTTTCATTTGAGGGGAGATCTCACCAAAATATGCTTTTCATGGTTCA 4020
Db 3961 TTGGCATTTTATCTTTCATTTGAGGGGAGATCTCACCAAAATATGCTTTTCATGGTTCA 4020
QY 4021 TTGTGTTTATTTAAATTTCTGTGATGCATATCTCAGGTTTACTTTAAACCTAGTCTATAGAT 4080
Db 4021 TTGTGTTTATTTAAATTTCTGTGATGCATATCTCAGGTTTACTTTAAACCTAGTCTATAGAT 4080
QY 4081 TCAAGATATCCCGTGTCAGGTCTCTAAAAGTAAAGAAAGAAATGGGTACTTGTGAAGGC 4140
Db 4081 TCAAGATATCCCGTGTCAGGTCTCTAAAAGTAAAGAAAGAAATGGGTACTTGTGAAGGC 4140
QY 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTGCCTTGTGTATTCACAAATATCAACGTGA 4200
Db 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTGCCTTGTGTATTCACAAATATCAACGTGA 4200
QY 4201 GCATCAGATAAGATTTCTTTAGTCACACACACACTCTCTTACTAGGAGATCCATAT 4260
Db 4201 GCATCAGATAAGATTTCTTTAGTCACACACACACTCTCTTACTAGGAGATCCATAT 4260
QY 4261 ACTTGAATAATTTGTTCTGCTTGACCCAGGTTTACTTATCAGTCCCTTTATTAATAATTTG 4320
Db 4261 ACTTGAATAATTTGTTCTGCTTGACCCAGGTTTACTTATCAGTCCCTTTATTAATAATTTG 4320
QY 4321 TAAATATTTGGGCTCGAGACCGGAGCGAGCTGGTTGAGTCTTCAAAAGTCCTAAACGTG 4380
Db 4321 TAAATATTTGGGCTCGAGACCGGAGCGAGCTGGTTGAGCTTCAAAAGTCCTAAACGTG 4380
QY 4381 CGGCGCTGGGTTCCGAGTTTATTCATTTGAATTCGGCTGGC - ACGAGAGCTCTGCAGAC 4438
Db 4381 CGGCGCTGGGTTCCGAGTTTATTCATTTGAATTCGGCTGGC - ACGAGAGCTCTGCAGAC 4438
QY 4439 AGAGAGCGCAGAGATGGAGATGGCAGCGGATTCATTCAGAGCTCGCGAACAGGCGC 4498
Db 4441 AGAGAGCGCAGAGATGGAGATGGCAGCGGATTCATTCAGAGCTCGCGAACAGGAGCG 4500
QY 4499 CCTCTGATGTAAGAAGACTTCCCTCGACAAACAGTCCGGTGAATGAAGGCAAACTCGAAG 4558
Db 4501 CCTCTGATGTAAGAAGACTTTCCTCGACAAACAGTCCGGTGAATGAAGGCAAACTCGAAG 4560
QY 4559 CCCTCAGAGTGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCT 4618
Db 4561 CCCTCAGAGTGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCT 4620
QY 4619 CAATCTCAGACTTACCAAGTTA - - - AAGTTGAGAAAGCTTGAAC - - - - - AGAG 4666
Db 4621 CAATCGCAAACTTACCAAAAGTTAAACAACTTAAGAAGCTTGAAC - - - - - AGAG 4680
QY 4667 TCTCAGGGGCGCTCGAGTATTCGCAAGAAAGTGTCCAAACCTCACCGATCTATATTTAA 4726
Db 4681 TCTCAGGGGCGCTCGAGTATTCGCAAGAAAGTGTCCGAAAGCTCACCGATCTAAATTTAA 4740
QY 4727 GTGCAACAAATTTAAAGACTCAGCAATAGAGCCACCTGAACAGTGTAGAAACCTCA 4786
Db 4741 GTGCAACAAATTTAAAGACTCAGCAATAGAGCCACCTGAACAGTGTAGAAACCTCA 4800
QY 4787 AGAGCTTAGAGCTTTCAATTTGAGGAGTAAACCAACCTGAACGACTACGAGAAACCTGT 4846

Db 4801 AGAGCTTAGACCTTTTCAATTTGGAGGTAAACCAACCTGAACGACTACCCAGAAATGTGT 4860
QY 4847 TCAAGCTTCTCTGCAACTCACAATATCTCGACAGCTGTTACTGGGGACCAACAGAGAGGCC 4906
Db 4861 TCAAGCTTCTCTGCAACTCACAATATCTCGACAGCTTATGACCGGACGACAAGAGGCC 4920
QY 4907 CTTTACTCAGATTTTGAAGACCACTGAGGCGCTGATCAGGAGGAGGAGGCTGAGCAGTG 4966
Db 4921 CTGACTCGGATGCTGAGGCTAGCTGGAGGCGCTGATGATGAGGAGGA - GATGAGAGTG 4979
QY 4967 AGGAGGAGTATGATGAAGATGCTCAGTGTGGAAGATGAGGAGGCGGAGGAGGAGG 5026
Db 4980 AGGAGGAGTATGATGAAGATGCTCAGTGTGGAAGACGAGGAGGAGGATGANGNG 5039
QY 5027 AGGAAGGTGAAGAGGAGGAGCTGAGTGGAGGGACGAGGAGGATGAAGAAGGTTATAAGC 5086
Db 5040 AGGAAGGTGAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGATGAAGAAGGTTATAAGC 5099
QY 5087 ATGGAGAGGTAGATGCGGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTCA 5146
Db 5100 ATGGAGAGGTAGATGACGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTCA 5159
QY 5147 AGCGAAATTCAGAACCTGAAGATGAGGAGAGATGATGACTAAAGTAGAATACCTATTT 5206
Db 5160 AGCGAAATTCAGAACCTGAAGATGAGGAGAGATGATGACTAAAGTAGAATACCTATTT 5219
QY 5207 TGAATAATTCCTATTTGATTTGACTGTTTACCCTATATCCCT - - - - - CCCCCCTCC 5260
Db 5220 TGAATAATTCCTATTTGATTTGACTGTTTACCCTATATCCCTCTCCCCCCCCCTCC 5279
QY 5261 AATCCTGCCCTGAACTTACTTTTTCTGTGTAACATTTCTGTGGGAATGAGACGG 5320
Db 5280 AATCCTGCCCTGAACTTACTTTTTCTGTGTAACATTTCTGTGGGAATGAGACGG 5339
QY 5321 GAAAGTGTACTGGGGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5380
Db 5340 GAAGAGTGTACTGGGGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5399
QY 5381 TTTTCTACTGCCAAATAAATAATTTTGAATAATTTAACTGGGATAGTACTAGCTTT 5434
Db 5400 TTTTCTACTGCCCTCTTATTTTTTTTCCCTACTTTTTTCTGTGTCGCGGTTTT 5453

RESULT 3

US-09-976-594-207
; Sequence 207, Application us/09976594
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROI
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 207
; LENGTH: 3955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1041138.7
; NAME/KEY: unsure
; LOCATION: 2235, 2268
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-207

Query Match 42.2%; Score 2441.2; DB 36; Length 3955;
Best Local Similarity 95.9%; Pred. No. 6e-207;
Matches 2542; Conservative 0; Mismatches 90; Indels 18; Gaps 3;

QY	2803	TCAGAGGTTGATTTGATGTCAGTGGGTAGATGAATTTGGGAGCAAAACAAGAT	2862
Db	1	TCAGAGGTTTGATTTGATGTCAGTGGGTAGATGAATTTGGGAGCAAAACAAGAT	60
QY	2863	AGAGTTCATGACAGTGAAGTTTATTTGATAGCTATATAAAGAAATGTTGAAGGT	2922
Db	61	AGAGTTCATGACAGTGAAGTTTATTTGATAGCTATATAAAGAAATGTTGAAGGT	120
QY	2923	TTGAATCCATTAGTGGCAGTAAAGGTTACAGAACGAAACTATTTGAGAAAGTACACAAG	2982
Db	121	TTGAATCCATTAGTGGCAGTAAAGGTTACAGAACGAAACTATTTGAGAAAGTACACAAG	180
QY	2983	GCAAGTCCTTACCTCAAGGCAGTTTATGTAAGCTCAATTCATGTCAGTGTCTTGCT	3042
Db	181	GCAAGTCCTTACCTCAAGGCAGTTTATGTAAGCTCAATTCATGTCAGTGTCTTGCT	240
QY	3043	ATGCTGGGTTATAGGATTTGGAACATATGATCAATCTGAGCACACATCAGTAACGTGAA	3102
Db	241	ATGCTGGGTTATAGGATTTGGAACATATGATCAATCTGAGCACACATCAGTAACGTGAA	300
QY	3103	TAGGATTTATAAATCCACAAGCATTTTACTAGTGAATCTGTGATATTTTCTAGCTACT	3162
Db	301	TAGGATTTATAAATCCACAAGCATTTTACTAGTGAATCTGTGATATTTTCTAGCTACT	360
QY	3163	CTTGCTGTGTTTATTTGAATCTTTTGCTCATATCCTATAGTAAGATTCAGGAAATATA	3222
Db	361	CTTGCTGTGTTTATTTGAATCTTTTGCTCATATCCTATAGTAAGATTCAGGAAATATA	420
QY	3223	TTTTTATTTGCTAGCAATTTAGCCCTTTTAGTCTTTTGAATCTATGCTCATATCTTAT	3282
Db	421	TTTTTATTTGCTAGCAATTTAGCCCTTTTAGTCTTTTGAATCTATGCTCATATCTTAT	480
QY	3283	AGTAAGAGTTTCAGGGAATGATTTCTATTTGCTCGGAATTTTAGCCCTTTCAGGTTTTCG	3342
Db	481	AGTAAGAGTTTCAGGGAATGATTTCTATTTGCTCGGAATTTTAGCCCTTTCAGGTTTTCG	540
QY	3343	AGCCCTCTTTTGTGTTAGGGACATAGTATGAGACAAAGATGAATGATCTATTCC	3402
Db	541	AGCCCTCTTTTGTGTTAGGGACATAGTATGAGACAAAGATGAATGATCTATTCC	600
QY	3403	AATTCACATGATGGGAAATGAACAAATAATGTTATTCACTCAAGGCTTCGCGCATGTT	3462
Db	601	AATTCACATGATGGGAAATGAACAAATAATGTTATTCACTCAAGGCTTCGCGCATGTT	660
QY	3463	TCCTGTGGAATTAAGGCTCAGACACAAATTTCCTAATGCCTGTGCTCAACTCTCAA	3522
Db	661	TCCTGTGGAATTAAGGCTCAGACACAAATTTCCTAATGCCTGTGCTCAACTCTCAA	720
QY	3523	TAGAACATATATTAATTTATCTTCTGAGTGTGTTTCCACAAATCCCATAGCCCTGT	3582
Db	721	TAGAACATATATTAATTTATCTTCTGAGTGTGTTTCCACAAATCCCATAGCCCTGT	780
QY	3583	GAAAAGATGTTTATAGGAAATATTAATTTAATATAGCATATTTGTCAATGTGGGACA	3642
Db	781	GAAAAGATGTTTATAGGAAATATTAATTTAATATAGCATATTTGTCAATGTGGGACA	840
QY	3643	TAGGACTAGTACCTGCTGAAAACCATCTCATGATCCTTGTGTGAAGAACTAATTCACACTA	3702
Db	841	TAGGACTAGTACCTGCTGAAAACCATCTCATGATCCTTGTGTGAAGAACTAATTCACACTA	900
QY	3703	GAAATACATATTTCTTGCTCAATTAACATAAATGTCAGAAAGTAAATAATATTC	3762
Db	901	GAAATACATATTTCTTGCTCAATTAACATAAATGTCAGAAAGTAAATAATATTC	960
QY	3763	CCTCTTAATAACATACATGCACTCAATTTTATTTTCTTACCCTGCGGTATCTAA	3822
Db	961	CCTCTTAATAACATACATGCACTCAATTTTATTTTCTTACCCTGCGGTATCTAA	1020
QY	3823	ACCTAGTTAGATACCTTTGTTTATGTTATTAATCTGACAGAACATACAAACGATCAC	3882
Db	1021	ACCTAGTTAGATACCTTTGTTTATGTTATTAATCTGACAGAACATACAAACGATCAC	1080
QY	3883	ATTGTGAGTCAGAGTGGAAATTCATTAATTCATGATACCAATAAAGATAGATTTA	3942
Db			
Db	1081	ATTGTGAGTCAGAGTGGAAATTCATTAATTCATGATACCAATAAAGATAGATTTA	1140
QY	3943	GCATTTTACAGGATGTTTGGCATTTTCTTTTCATTTGAGGGGAGATCTCACCAAAA	4002
Db	1141	GCATTTTACAGGATGTTTGGCATTTTCTTTTCATTTGAGGGGAGATCTCACCAAAA	1200
QY	4003	TATGTCCTTTCATGTTTCATTTGTTTAAATTTCTGTGATGATATCTCAGGTTTACT	4062
Db	1201	TATGTCCTTTCATGTTTCATTTGTTTAAATTTCTGTGATGATATCTCAGGTTTACT	1260
QY	4063	TAAACCTAGTCTATAGATTCAAGAGATATCCCGTGTGAGTCTCTAAAGTAAAGAAAAA	4122
Db	1261	TAAACCTAGTCTATAGATTCAAGAGATATCCCGTGTGAGTCTCTAAAGTAAAGAAAAA	1320
QY	4123	ATGGGTACTTGTCAAGGCTGATTACAGTAAGTGTGTAGAGGGAGTGCCTTGTGTATT	4182
Db	1321	ATGGGTACTTGTGAAGGCTGATTACAGTAAGTGTGTAGAGGGAGTGCCTTGTGTATT	1380
QY	4183	CACAAATTTATCAACGTCAGCATCAGATAAGATTTTCTTTAGTCACACACACCTTCTCT	4242
Db	1381	CACAAATTTATCAACGTCAGCATCAGATAAGATTTTCTTTAGTCACACACACCTTCTCT	1440
QY	4243	TACTAGAAAGATCCATATACTTGAATTAATTTGCTTGCCTTGACCCAGGTTTACTTATCAGTC	4302
Db	1441	TACTAGAAAGATCCATATACTTGAATTAATTTGCTTGCCTTGACCCAGGTTTACTTATCAGTC	1500
QY	4303	CCTTTATTTAATTAATTTGTAATATTGGGCTCGAAGCCGAGCGGAGTGGTGTGAGTCT	4362
Db	1501	CCTTTATTTAATTAATTTGTAATATTGGGCTCGAAGCCGAGCGGAGTGGTGTGAGTCT	1560
QY	4363	TCAAAGTCCTTAAACGTCGCGGCTGAGGTTTTCAGGTTTATTTGATTAATTCGCGTGGCAC	4422
Db	1561	TCAAAGTCCTTAAACGTCGCGGCTGAGGTTTTCAGGTTTATTTGATTAATTCGCGGCTGG	1620
QY	4423	GAGAGCTCTGACAGACAGAGCGCGAGATGGAGATGGGACAGCGGATTCATTCAGAG	4482
Db	1621	GAGAGCTCTGACAGACAGAGCGCGAGATGGAGATGGGACAGCGGATTCATTTAGAG	1680
QY	4483	CTCGGAAACAGGGCGCCTCTGATGTGAAGAACTTGCCTTGACACACAGTCCGTCGAAT	4542
Db	1681	CTCGGAAACAGGGCGCCTCTGATGTGAAGAACTTGCCTTGACACACAGTCCGTCGAAT	1740
QY	4543	GAAGGCAAACTCGAAGCCCTCAGATGAATTTGAAGAACTGGAATCTTAAGTAAATC	4602
Db	1741	GAAGGCAAACTCGAAGCCCTCAGATGAATTTGAAGAACTGGAATCTTAAGTAAATC	1800
QY	4603	AACGAGGCTCACCTCAATCTCAGACTTACCAAGTTA--AAGTTGAGAAAGCTTGAA	4659
Db	1801	AACGAGGCTCACCTCAATCTCAGACTTACCAAGTTA--AAGTTGAGAAAGCTTGAA	1860
QY	4660	CTA-----AGAGTCTCAGGGGCTGGAAGTATTTGGCAGAAAAGTCTCCAAACCTC	4710
Db	1861	CTAAGCCATACAGAGTCTCAGGGGCTGGAAGTATTTGGCAGAAAAGTCTCCGAACTC	1920
QY	4711	ACGATCTATTTAAGTGGCAACAAAATTTAAAGACTCAGCACTAGCAGCAATAGAGCACTGAAA	4770
Db	1921	ACGATCTATTTAAGTGGCAACAAAATTTAAAGACTCAGCACTAGCAGCAATAGAGCACTGAAA	1980
QY	4771	CAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTTGGAGGTAACCACTGAAAGC	4830
Db	1981	AGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTTGGAGGTAACCACTGAAAGC	2040
QY	4831	TACGGAGAAAACCTGTTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTTCTACTGG	4890
Db	2041	TACGGAGAAAACCTGTTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTTCTACTGG	2100
QY	4891	GACCAAGAGGCCCCCTTACTCAGATATTTAGAGACACCGTGGAGGCCCTGGATGACGAG	4950
Db	2101	GACCAAGAGGCCCCCTTACTCAGATATTTAGAGACACCGTGGAGGCCCTGGATGACGAG	2160
QY	4951	GAGGAGGCTGAGCATGAGGAGGATGATGAAGATGCTCAGTCTAGTGGAGATGAGGAG	5010
Db			

Db 2161 GAGGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAGACGAGGAG 2220
QY 5011 GCGGAGGAGGAGGAGGAGGTGAAGAGGAGGACGTGAGTGGAGGGACGAGGAGGAT 5070
Db 2221 GACGAGGATGAGGANGAGGAGGTGAAGAGGAGGACGTGAGTGGAGANGAGGAGGAT 2280
QY 5071 GAAGAAGGTTATACGATGGAGAGGTAGATGGCCAGGAAGATGAAGAAGAGCTTGGTGAA 5130
Db 2281 GAAGAAGGTTATACGATGGAGAGGTAGATGACGAGGAAGATGAAGAAGATGACTAA 2340
QY 5131 GAAGAAGGGGTGAGAACGGAATGAGAACCTGAAGATGAGGAGGAAGATGACTAA 5190
Db 2341 GAAGAAGGGGTGAGAACGGAATGAGAACCTGAAGATGAGGAGGAAGATGACTAA 2400
QY 5191 GTAGAATAACCTATTTTGAATAATCCTATTGTGATTTGACTGTTTACCCTATATCCCC 5250
Db 2401 GTGGAATAACCTATTTTGAATAATCCTATTGTGATTTGACTGTTTACCCTATATCCCC 2460
QY 5251 T-----CCCCCCTCCAATCCTGCCCCCTGAAACTTACTTTTTCTGATTTGAACATTCG 5304
Db 2461 TCTCCCCCCCCCTCCAATCCTGCCCCCTGAAACTTATTTTCTGATTTGAACATTCG 2520
QY 5305 TGTGGGAATGAGACGGGAAAAGTGTACTGGGGGTGTGGAGGGAGGAGGCGAGGGCG 5364
Db 2521 TGTGGGAACGAGAGGGGAAGAGTGTACTGGGGGTGTGGAGGGAGGAGGCGAGGGCG 2580
QY 5365 GTGACTAAAAATACTATTTTACTGCCAAATAAAAAATAATTTGTAATAATTAACTGGGA 5424
Db 2581 GTGGAATAAATACTATTTTACTGCCACTTTATTTTTCCTCCCTACTTTTCTTTCTTGT 2640
QY 5425 TACTAGCTTT 5434
Db 2641 GTCCGGTTTT 2650

RESULT 4
US-60-240-409-207
; Sequence 207, Application US/60240409
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny L.
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 P
; CURRENT APPLICATION NUMBER: US/60/240,409
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 207
; LENGTH: 3955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 1041138.7
; NAME/KEY: unsure
; LOCATION: 2235, 2268
; OTHER INFORMATION: a, t, c, g, or other
US-60-240-409-207

Query Match 42.2%; Score 2441.2; DB 68; Length 3955;
Best Local Similarity 95.9%; Pred. No. 6e-207;
Matches 2542; Conservative 0; Mismatches 90; Indels 18; Gaps 3;
QY 2803 TGTAGAAGTTTGATTTTGATGTCAGTGTGGTGAATCAATTTGTGGGAAGCAAAACAAGAT 2862
Db 1 TGTAGAAGTTTGATTTTGATGTCAGTGTGGTGAATCAATTTGTGGGAAGCAAAACAAGAT 60
QY 2863 AGAGTTCAATGACAGTGAAGAGTTTATTTGCTATAAGCTATATAAACAAGATTTGAAGGT 2922
Db 61 AGAGTTCAATGACAGTGAAGAGTTTATTTGCTATAAGCTATATAAACAAGATTTGAAGGT 120
QY 2923 TTGAATCCATTAGTGGCAGTAAAGGTGTACAGCAAGCAATTTTGAAGTACACAG 2982

Db 121 TTGAATCCATTAGTGGCAGTAAAGGTGTACAGACGAACCACTATTTTGAGAAGTACACAAG 180
QY 2983 GCAAGTCTTACTTTCAAGGCAGTTTATGTAAAGCTCATTTCAATTTGCTCAGTGTCTTCTTGT 3042
Db 181 GCAAGTCTTACTTTCAAGGCAGTTTATGTAAAGCTCATTTCAATTTGCTCAGTGTCTTCTTGT 240
QY 3043 ATGTGTGGGTTATAGGATTTGGAACATATGATCAATCTGAGCACACATCAGTAAACTGAA 3102
Db 241 ATGTGTGGGTTATAGGATTTGGAACATATGATCAATCTGAGCACACATCAGTAAACTGAA 300
QY 3103 TAGGATTATTAATAATCCACAAGCATTTTACTAGTGAATCTGTGATATTTTCTAGCTACT 3162
Db 301 TAGGATTATTAATAATCCACAAGCATTTTACTAGTGAATCTGTGATATTTTCTAGCTACT 360
QY 3163 CTGTGCTGTTTTATTGTGAATCTTTTGTCTCATATCCTATAGTAAAGATTTTCAGAAATATA 3222
Db 361 CTGTGCTGTTTTATTGAAATCTTTTGTCTCATATCCTATAGTAAAGATTTTCAGAAATATA 420
QY 3223 TTTTATTTTGCCTAGAAATTTTGTAGCCTTTTGTAGTAAAGATTTTGTGAATCTATTTGCTCATATTTCTTAT 3282
Db 421 TTTTATTTTGCCTAGAAATTTTGTAGCCTTTTGTAGTAAAGATTTTGTGAATCTATTTGCTCATATTTCTTAT 480
QY 3283 AGTAAGAGTTTCAGGGAATGTATTTCTATTTCTGTGGAATTTTGTAGCCTTTTCAGGTTTTTG 3342
Db 481 ACTAAGAGTTTCAGGGAATGTATTTCTATTTCTGTGGAATTTTGTAGCCTTTTCAGGTTTTTG 540
QY 3343 AGCCCTCTTTTGTCTTATGGGACATAGTATGAGACAAAGATGAATGATCTTCTATTTCCC 3402
Db 541 AGCCCTCTTTTGTCTTATGGGACATAGTATGAGACAAAGATGAATGATCTTCTATTTCCC 600
QY 3403 AATTCACATGATGGGAAATGAAGCAAAATGTTTATTCACTCAGGCTTCTGCCATGTT 3462
Db 601 AATTCACATGATGGGAAATGAAGCAAAATGTTTATTCACTCAGGCTTCTGCCATGTT 660
QY 3463 TCCTGTGGAATTCAGGCTCAGACACAAATTTCTTAATAGCCTGTCTCCTAACTTCTCAA 3522
Db 661 TCCTGTGGAATTCAGGCTCAGACACAAATTTCTTAATAGCCTGTCTCCTAACTTCTCAA 720
QY 3523 TGAACACATATTAATTTATCTTCTCCTGAGTGTCTTCCACAAATCCCATAGCCTGT 3582
Db 721 TGAACACATATTAATTTATCTTCTCCTGAGTGTCTTCCACAAATCCCATAGCCTGT 780
QY 3583 GAAAAAGATTTGTTTAGGAAATATTTTAAATATAGCATATTTTGTCAATGTGGGACA 3642
Db 781 GAAAAAGATTTGTTTAGGAAATATTTTAAATATAGCATATTTTGTCAATGTGGGACA 840
QY 3643 TAGGACTAGTACCTGCTGAAACCATCTCATGATCCTTGTGTAAGAACTAATTCACACTA 3702
Db 841 TAGGACTAGTACCTGCTGAAACCATCTCATGATCCTTGTGTAAGAACTAATTCACACTA 900
QY 3703 GAAATACTATTTTCTCTGCTCATTAATAAACATAAATGTCTCAGAAAGTAAAAATTTATTC 3762
Db 901 GAAATACTATTTTCTCTGCTCATTAATAAACATAAATGTCTCAGAAAGTAAAAATTTATTC 960
QY 3763 CTCCTAAATAAACATACATGCCACTCAAAATTTTATTCCTTACCACCTTGGCGTATCTAA 3822
Db 961 CTCCTAAATAAACATACATGCCACTCAAAATTTTATTCCTTACCACCTTGGCGTATCTAA 1020
QY 3823 ACCTAGTTAGATACHTTGGTTTTTAGGTATAATCTGACAGAACAGATACAAACAGATCAC 3882
Db 1021 ACCTAGTTAGATACHTTGGTTTTTAGGTATAATCTGACAGAACAGATACAAACAGATCAC 1080
QY 3883 ATGTGAGTCAAGAGTGAAGAAATTCATAATTCATGATGATACCAATAAAGATAGATTTA 3942
Db 1081 ATGTGAGTCAAGAGTGAAGAAATTCATAATTCATGATGATACCAATAAAGATAGATTTA 1140
QY 3943 GCTTTTACAGGATGTTTTTGGCATTTTATTTCTTCTCATTTTGGGGGAGATCTCACCAAAA 4002
Db 1141 GCTTTTACAGGATGTTTTTGGCATTTTATTTCTTTTCAATTTGAGGGGAGATCTCACCAAAA 1200
QY 4003 TATGCTTTTCAATGTTTCAATGTTTATTTAAATTTCTGTGATGATATTTCTCAGGTTACTT 4062
Db 1201 TATGCTTTTCAATGTTTCAATGTTTATTTAAATTTCTGTGATGATATTTCTCAGGTTACTT 1260


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Qy 4063 TAAACCTAGTCTATAGATTCAAAGATATCCCGTGTCAAGTCTCTAAAGATGAAAAAGAAAA 4122
Db 1261 TAAACCTAGTCTATAGATTCAAAGATATCCCGTGTCAAGTCTCTAAAGATGAAAAAGAAAA 1320
Qy 4123 ATGGGTACTTGTGAAGGCTGATTCACAGTAAGTGTAGTGTAGAGGGAGTGCCTTGTGTATT 4182
Db 1321 ATGGGTACTTGTGAAGGCTGATTCACAGTAAGTGTAGTGTAGAGGGAGTGCCTTGTGTATT 1380
Qy 4183 CACAAATTTATCAACGTGAGCATCAGATAGATTTCCTTTAGTTCACACACACTACCTTCT 4242
Db 1381 CACAAATTTATCAACGTGAGCATCAGATAGATTTCCTTTAGTTCACACACACTACCTTCT 1440
Qy 4243 TACTAGGAAGATCCATATACATTTGAATAATGTCTCTGTGACCCAGAGTGTACTTATCAGTC 4302
Db 1441 TACTAGGAAGATCCATATACATTTGAATAATGTCTCTGTGACCCAGAGTGTACTTATCAGTC 1500
Qy 4303 CCTTTATTAATAATTTGTAAATATTTGGGGCTCGAGAACCCAGCGGAGCTGGTTGAGTCT 4362
Db 1501 CCTTTATTAATAATTTGTAAATATTTGGGGCTCGAGAACCCAGCGGAGCTGGTTGAGCCT 1560
Qy 4363 TCAAAGTCTCTAAACGTGCGGCCGTGGTTCGAGGTTTATTGATGAAATTCGGCTGGCAC 4422
Db 1561 TCAAAGTCTCTAAACGTGCGGCCGTGGTTCGAGGTTTATTGATGAAATTCGGCGGGCGC 1620
Qy 4423 GAGAGCCTCTGCAGACAGAGCGCGAGAGATGGAGATGGGCGAGACGGATTCATTCAGAG 4482
Db 1621 GGGAGCCTCTGCAGAGAGAGCGCGAGAGATGGAGATGGGCGAGACGGATTCATTTAGAG 1680
Qy 4483 CTGCGGAACAGGGCGCCTCTCTGATGTGAAGAACCTTGCCCTGGGACCAACAGTCGGTCGAAT 4542
Db 1681 CTGCGGAACAGGACGCCCTCTCTGATGTGAAGAACCTTGCCCTGGGACCAACAGTCGGTCGAAT 1740
Qy 4543 GRAGGCARACTCGAGCCCTCAGAGTGAATTTGAAGAACTGGAATCTTAAAGTAAATATC 4602
Db 1741 GAAGGCAAACTCGAAGGCCCTCAGAGTGAATTTGAAGAACTGGAATCTTAAAGTAAATATC 1800
Qy 4603 AACGGAGGCTCACCTCAATCTCAGACTTTACCAAAGTTA ---AAGTTGAGAAAGCTTGAA 4659
Db 1801 AAGCTAGGCTCACCTCAATCTCAGAACTTTACCAAAGTTAAGAAAGCTTGAA 1860
Qy 4660 CTA-----AGAGTCTCAGGGGCCCTGGGAAGTATTTGGCGAGAAAGTGTCCAAACCTC 4710
Db 1861 CTAAGCGATAACAGAGTCTCAGGGGCCCTGGAAGTATTTGGCGAGAAAGTGTCCGAACCTC 1920
Qy 4711 ACSCTATATTTAAGTGCACAAATAAATAAGACCTCAGCACAAATAGAGCCTAGAA 4770
Db 1921 ACGCATCTAAATTTAAGTGCACAAATAAATAAGACCTCAGCACAAATAGAGCCTAGAA 1980
Qy 4771 CAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTTGCGAGGTAAACCAACCTGAACGAC 4830
Db 1981 AAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTTGCGAGGTAAACCAACCTGAACGAC 2040
Qy 4831 TAGCGAGAAAACCTGTTCAAGCTTCTCCTGCACTACATATCTCGACAGCTGTTACTTGG 4890
Db 2041 TACCGAGAAAATGTGTTCAAGCTTCTCCTGCACTACATATCTCGACAGCTGTTACTTGG 2100
Qy 4891 GACCACAAGGAGGCCCTTACTCAGATATTTGAGGACCACTGGAGGCCCTGGATGACGAG 4950
Db 2101 GACGACAAGGAGGCCCTGACTCGGATGCTGAGGCTAGCTGGAGGCCCTGGATGATGAG 2160
Qy 4951 GAGGAGGGTGAAGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAG 5010
Db 2161 GAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAG 2220
Qy 5011 GGCAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAG 5070
Db 2221 GAGGAGGATGAGGAGGAGGAGGAGTGAAGGAGGAGGAGGAGTGAAGGAGGAGGAGGAG 2280
Qy 5071 GAAGAAGCTTATACGATGAGGAGGAGTGAAGGAGGAGGAGTGAAGGAGGAGGAGTGAAG 5130
Db 2281 GAAGAAGCTTATACGATGAGGAGGAGTGAAGGAGGAGGAGTGAAGGAGGAGGAGTGAAG 2340
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Qy 5131 GAAGAAGGGGTGAGAGCGCAAAATGAGAACCTGAGAGATGAGGGAGAGATGATGACTAA 5190
Db 2341 GAAGAAGGGGTGAGAGCGCAAAATGAGAACCTGAGAGATGAGGGAGAGATGATGACTAA 2400
Qy 5191 GTAGATAACCTATTTGAAAATTCCTATTGTGATTTGACTGTTTTACCCATATCCCC 5250
Db 2401 GTGGAATAACCTATTTGAAAATTCCTATTGTGATTTGACTGTTTTACCCATATCCCC 2460
Qy 5251 T-----CCGCCCTCCAATCCTGCCCTGAAACTTTACTTTTTCTGTGATTTGAACATTCG 5304
Db 2461 TCTCCCCCCCCCTCCANTCTGCCCTGAACTTATTTTTCTGATTTGTAACGTTGC 2520
Qy 5305 TGTGGGAATGAGACGGGAAAGTGTACTGCGGGGTTGTGAGGAGGAGGAGGAGGAGGCG 5364
Db 2521 TGTGGGAACGAGAGGGGAAGAGTGTACTGCGGGGTTGCGGGGGGAGGAGTGGCGGTGGG 2580
Qy 5365 GTGACTAAATACTATTTTACTGCAATAAAATAAATAATTTGTAATAATTAACATGGGA 5424
Db 2581 GTGGAATAAATACTATTTTACTGCCACTCTTATTTTTTCCCTACTTTTCTTTGT 2640
Qy 5425 TACTAGCTTT 5434
Db 2641 GTCGGGTTTT 2650

RESULT 5
US-09-760-469-94
; Sequence 94, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; PRIORITY DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-760-469-94

Query Match 16.08; Score 925.6; DB 30; Length 1197;
Best Local Similarity 91.7%; Pred. No. 3.5e-73;
Matches 1016; Conservative 0; Mismatches 74; Indels 18; Gaps 3;
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Db 393 GGCCTGGAAGTATTGGCAGAAAAAGTCCGAAACCTCAGCATCTAAATTTAAGTGGCAAC 452
QY 4735 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAAACCTCAAGAGCTTA 4794
Db 453 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAAAGTGTAGAAAAACCTCAAGAGCTTA 512
QY 4795 GACCTTTTCAATTGCGAGGTAAACAACTGAACGACTACGAGAAAAACGTTTCAAGCTT 4854
Db 513 GACCTTTTCAATTGCGAGGTAAACAACTGAACGACTACGAGAAAAATGTTTCAAGCTT 572
QY 4855 CTCCTGCAACTACATATCTCGACAGCTGTTACTTGGACCAACAGGAGGCCCTTACTCA 4914
Db 573 CTCCTGCAACTACATATCTCGACAGCTGTTACTTGGACCAACAGGAGGCCCTTACTCG 632
QY 4915 GATATTGAGGACCGTGGAGGCTCGATCAGGAGGAGGAGGCTGAGCATGAGGAGGAG 4974
Db 633 GATCTGAGGCTACGTGGAGGCTCGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 692
QY 4975 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGT 5034
Db 693 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGT 752
QY 5035 GAAGAGGAGGAGGAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGGAGAG 5094
Db 753 GAAGAGGAGGAGGAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGGAGAG 812
QY 5095 GTAGATGGCAGGAGGAGTGAAGAGAGCTTGGTGAAGAAAGGGTCAAGAGCGGAAAA 5154
Db 813 GTAGATGGCAGGAGGAGTGAAGAGAGCTTGGTGAAGAAAGGGTCAAGAGCGGAAAA 872
QY 5155 TGAAACCTGAAGATGAGGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 5214
Db 873 CGAAGACCTGAAGATGAGGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 932
QY 5215 TCCTATTGATTTGATGTTTACCCATATCCCTTACCCCTTACCCCTTACCCCTTACCCCT 5268
Db 933 TCCTATTGATTTGATGTTTACCCATATCCCTTACCCCTTACCCCTTACCCCTTACCCCT 992
QY 5269 CCCCTGAAACTTACTTTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGAT 5328
Db 993 CCCCTGAAACTTACTTTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGAT 1052
QY 5329 TACTGGGGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5388
Db 1053 TACTGGGGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1112
QY 5389 GCCAAATAAATAATATTCTGAATATTA 5418
Db 1113 GCCAAATAAATAATATTCTGAATATTA 1142

RESULT 6

US-10-216-583-94

; Sequence 94, Application US/10216583
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254CIN
; CURRENT APPLICATION NUMBER: US/10/216,583
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,469
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963

; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-583-94

Query Match 16.0%; Score 925.6; DB 42; Length 1197;
Best Local Similarity 91.7%; Pred. No. 3.5e-73;

Matches 1018; Conservative 0; Mismatches 74; Indels 18; Gaps 3;

QY 4327 TTGGGGCTCGAGAACCGAGCGAGCTGTTGAGTCTTCAAAGTCTCTAAACGTTGGCGCG 4386
Db 33 TGGGGCTCGAGAACCGAGCGAGCTGTTGAGCTTCAAAGTCTCTAAACGTTGGCGCG 92
QY 4387 TGGGTTTCGAGCTTTATTGATTGAATTCGGCTGCGAGGAGCCTCTGCAGACAGAGCG 4446
Db 93 TGGGTTTCGAGCTTTATTGATTGAATTCGGCTGCGAGGAGCCTCTGCAGACAGAGCG 152
QY 4447 CGAGAGATCGAGATGGCAGACGAGATTCAATTCAGAGCTCGCGAACAGGCGCCCTCTGAT 4506
Db 153 CGAGAGATCGAGATGGCAGACGAGATTCAATTCAGAGCTCGCGAACAGGAGCCCTCTGAT 212
QY 4507 GTGAAAGAACTTCCCTCGACAACTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4566
Db 213 GTGAAAGAACTTCCCTCGACAACTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 272
QY 4567 GATGAATTTGAAGAACTGCAATTTTAAGTAAATCAACGAGGAGCCTCACCTCAATCTCA 4626
Db 273 GATGAATTTGAAGAACTGCAATTTTAAGTAAATCAACGAGTGAAGTGAAGTGAAGTGAAG 332
QY 4627 GACTTACCAAAAGTTAAAGT---TGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4674
Db 333 AACTTACCAAAAGTTAAACAACTTAAGAGCTTGAACCTAAGCGATAACAGAGTCTCAGGG 392
QY 4675 GGCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAAC 4734
Db 393 GGCCTGGAAGTATTGGCAGAAAGTGTCCGAACTCAGCATCTAAATTTAAGTGGCAAC 452
QY 4735 AAAATTAAAGACCTCAGACCAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTA 4794
Db 453 AAAATTAAAGACCTCAGACCAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTA 512
QY 4795 GACCTTTTCAATTGCGAGGTAACCAACCTGAACGACTACGGAGAAAAAGTGTTCAGCTT 4854
Db 513 GACCTTTTCAATTGCGAGGTAACCAACCTGAACGACTACGGAGAAAAATGTTGTTCAAGCTC 572
QY 4855 CTCCTGCAACTACATATCTCGACAGCTGTTACTGGACCAACAGGAGGCCCTTACTCA 4914
Db 573 CTCCTGCAACTACATATCTCGACAGCTGTTACTGGACCAACAGGAGGCCCTTACTCG 632
QY 4915 GATATTGAGGACCGTGGAGGCTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 4974
Db 633 GATGCTGAGGCTACGTGGAGGCTGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 692
QY 4975 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGT 5034
Db 693 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGT 752
QY 5035 GAAGAGGAGGAGGAGTGGAGGAGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGGAGAG 5094
Db 753 GAAGAGGAGGAGGAGTGGAGGAGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGGAGAG 812
QY 5095 GTAGATGGCAGGAGGAGTGAAGAGAGCTTGGTGAAGAAAGGGTCAAGAGCGGAAAA 5154


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; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-649-164-9117

Query Match          15.9%; Score 917.6; DB 25; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

QY 4327 TTGGGGCTCGAAGACCGAGCGAGCTGTTGAGTCTTCAAAAGTCTAAAAGTGCAGCGCG 4386
Db 196 TGGGGCTCGAAGACCGAGCGAGCTGTTGAGTCTTCAAAAGTCTAAAAGTGCAGCGCG 255

QY 4387 TGGGTTTCGAGGTTTATTTGATTTGAATTCGGCTGGCAGAGAGCTCTGCAGACAGAGCG 4446
Db 256 TGGGTTTCGAGGTTTATTTGATTTGAATTCGGCTGGCAGAGAGCTCTGCAGACAGAGCG 315

QY 4447 CGAGAGATGGAGATGGCAGCGGATTCATTCAGAGCTGCGGAACAGCGGCCCTCTGAT 4506
Db 316 CGAGAGATGGAGATGGCAGCGGATTCATTTAGAGCTGCGGAACAGCGGCCCTCTGAT 375

QY 4507 GTGAAGAAGCTTGGCCCTGGACAAACAGTCGGTGAAGTGAAGGCAAACTCGAAGCCCTCACA 4566
Db 376 GTGAAGAAGCTTGTCTCTGGACAAACAGTCGGTGAAGTGAAGGCAAACTCGAAGCCCTCACA 435

QY 4567 GATGAATTTGAGAACTGGAATTCCTTAAGTAAATCAACAGGAGCTCACCTCAATCTCA 4626
Db 436 GATGAATTTGAGAACTGGAATTCCTTAAGTAAATCAACAGGAGCTCACCTCAATCTCA 495

QY 4627 GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4674
Db 496 AACTTACCAAGTTAACAACAACTTAAAGAGCTTGAAGTGAAGGATAACAGAGTCTCAGGG 555

QY 4675 GGCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCGCATCTATATTAAGTGGCAAC 4734
Db 556 GGCCTGGAAGTATTGGCAGAAAGTGTCCGAACCTCAGCGCATCTAATTTAAGTGGCAAC 615

QY 4735 AAAATTAAGACCTTCACACAAATAGACCCACTGAACAGTTAGAAAACCTCAAGAGCTTA 4794
Db 616 AAAATTAAGACCTTCACACAAATAGACCCACTGAAAAGTTAGAAAACCTCAAGAGCTTA 675

QY 4795 GACCTTTTCAATTGCGAGGTAAACCAACTGAACGACTACGAGAAAAGCTGTTCAGCTT 4854
Db 676 GACCTTTTCAATTGCGAGGTAAACCAACTGAACGACTACGAGAAAAGTGTTCAGCTT 735

QY 4855 CTCTGCAACTCATAATCTCGACAGCTGTTACTGGGACCAAGAGGCGCCCTTACTCA 4914
Db 736 CTCCGCAACTCATAATCTCGACAGCTATGACCGGACCAAGAGGCGCCCTGACTCG 795

QY 4915 GATATTGAGACCACTGGAGGCGCTGGATGACGAGAGAGAGGCTGAGCATGAGGAGAG 4974
Db 796 GATGCTGAGGCGCTACCTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGAG 855

QY 4975 TATGATCAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGCT 5034
Db 856 TATGATCAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 915

QY 5035 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGCTTATACGATGGAGAG 5094
Db 916 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGCTTATACGATGGAGAG 975

QY 5095 GTAGATGCCAGAGATGAAGAGAGCTTGGTGAAGAGAGAGAGGCTCAGAGCGGAGG 5154
Db 976 GTAGATGCCAGAGATGAAGAGAGCTTGGTGAAGAGAGAGAGGCTCAGAGCGGAGG 1035

QY 5155 TGAGAACCTCAAGATGAGGAGAGAGATGATGACTAAGTGAAGTAACTATTTTGAAGAT 5214
Db 1036 CGAGAACCTCAAGATGAGGAGAGAGATGATGACTAAGTGAAGTAACTATTTTGAAGAT 1095
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QY 5215 TCCTATTGTGATTGACTGTTTTTACCATATCCCT-----CCCCCTCCAACTCTGC 5268
Db 1096 TCCTATTGTGATTGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCAACTCTGC 1155

QY 5269 CCCTGAAAACCTTACTTTTTTCTGATTGAACATTGCTGGGAATGAGACGGGAAAGTG 5328
Db 1156 CCCTGAAAACCTTACTTTTTTCTGATTGAACATTGCTGGGAATGAGACGGGAAAGTG 1215

QY 5329 TACTGGGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5388
Db 1216 TACTGGGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1275

QY 5389 GCCAAATAAAATAATTTGTAATTAATTAACCTGGGATAGCTTT 5434
Db 1276 GCCACTTTATTTTTTCCCTACTTTTTTCTTTGTGTCGGGTTTT 1321
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RESULT 9

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US-09-652-913-10130
; Sequence 10130, Application US/09652913
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean R.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1174-001
; CURRENT APPLICATION NUMBER: US/09/652,913
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,107
; NUMBER OF SEQ ID NOS: 10833
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10130
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-913-10130
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Query Match          15.9%; Score 917.6; DB 25; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;
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QY 4735 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGTAAACCTCAAGAGCTTA 4794
Db 616 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGTAAACCTCAAGAGCTTA 675
QY 4795 GACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGAGAGAAACGTTTCAAGCTT 4854
Db 676 GACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGAGAGAAATGTCTCAAGCTC 735
QY 4855 CTCCTGCAACTACATATCTCGACAGCTGTTACTGGGACCACAGGAGGCCCTTACTCA 4914
Db 736 CTCCTGCAACTACATATCTCGACAGCTGTTACTGGGACCACAGGAGGCCCTTACTCG 795
QY 4915 GATATTGAGACACCTGAGGCGCTTGTATGACGAGGAGGAGGCTGACATGAGGAGAG 4974
Db 796 GATGCTGAGGCTACGTGAGGCGCTTGTATGACGAGGAGGAGGCTGACATGAGGAGAG 855
QY 4975 TATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGT 5034
Db 856 TATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGT 915
QY 5035 GAAGAGGAGGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5094
Db 916 GAAGAGGAGGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 975
QY 5095 GTAGATGGCGAGGAAGATGAAGAGAGCTTGTGAAGAGAAAGGGTCAAGAGCGAAAA 5154
Db 976 GTAGATGGCGAGGAAGATGAAGAGAGCTTGTGAAGAGAAAGGGTCAAGAGCGAAAA 1035
QY 5155 TGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5214
Db 1036 CGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1095
QY 5215 TCCTATTGATGTTGACTGTTTACCCATATCCCT-----CCCCCTCCCAATCCTGC 5268
Db 1096 TCCTATTGATGTTGACTGTTTACCCATATCCCTCTCCCCCTCCCAATCCTGC 1155
QY 5269 CCCTGAAACTTACTTTTTCTGATTGAACATGCTGTGGAAATGAGACGGGAAAGTG 5328
Db 1156 CCCTGAAACTTACTTTTTCTGATTGAACATGCTGTGGAAATGAGACGGGAAAGTG 1215
QY 5329 TACTGGGGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5388
Db 1216 TACTGGGGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1275
QY 5389 GCCAAATAAATAATTTGTAATAATTAACCTGGATAGTACTTT 5434
Db 1276 GCCACTTTATTTTTTCCCTACTTTTCTTGTGTCGGGTTT 1321

RESULT 10
US-09-699-998-8868
; Sequence 8868, Application US/09699998
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2008-001
; CURRENT APPLICATION NUMBER: US/09/699,998
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,362
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 10905
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8868
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-699-998-8868

Query Match 15.9%; Score 917.6; DB 27; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;
QY 4327 TTGGGCTCGAGAACCGAGCGAGCTGGTGGTCTTCAAAGTCTTAAACGTCGGCGCG 4386
Db 196 TGGGGCTCGAGAACCGAGCGAGCTGGTGGTCTTCAAAGTCTTAAACGTCGGCGCG 255
QY 4387 TGGGTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTTCGACAGAGAGCG 4446
Db 256 TGGGTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTTCGACAGAGAGCG 315
QY 4447 CGAGAGATGAGATGGGCGAGCGATTCATTAGAGCTGCGGAACAGGACGCCCTCTGAT 4506
Db 316 CGAGAGATGAGATGGGCGAGCGATTCATTAGAGCTGCGGAACAGGACGCCCTCTGAT 375
QY 4507 GTGAAGAACTTCCCTGGACACAGTCGTCGAATGAAGGCAAACTCGAAGCCCTCACA 4566
Db 376 GTGAAGAACTTCCCTGGACACAGTCGTCGAATGAAGGCAAACTCGAAGCCCTCACA 435
QY 4567 GATGAATTTGAAGAACTTGAATTTAAAGTAAATCAACGAGGCGCTCACTCAATCTCA 4626
Db 436 GATGAATTTGAAGAACTTGAATTTAAAGTAAATCAACGAGGCGCTCACTCAATCTCA 495
QY 4627 GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4674
Db 496 AACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 555
QY 4675 GGCCTGGAAGTATGGCAGAAAGTGTCCAACTCAGCATCTATATTTAAAGTGCAC 4734
Db 556 GGCCTGGAAGTATGGCAGAAAGTGTCCAACTCAGCATCTATATTTAAAGTGCAC 615
QY 4735 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTA 4794
Db 616 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTA 675
QY 4795 GACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGAGAGAAACGTTTCAAGCTT 4854
Db 676 GACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGAGAGAAATGTGTTCAGCTC 735
QY 4855 CTCCTGCAACTACATATCTCGACAGCTGTTACTGGGACCACAGGAGGCCCTTACTCA 4914
Db 736 CTCCTGCAACTACATATCTCGACAGCTGTTACTGGGACCACAGGAGGCCCTTACTCG 795
QY 4915 GATATTGAGGACACGCTGGAGGCGCTGGATGACGAGGAGGAGGAGGAGGAGGAGGAG 4974
Db 796 GATGCTGAGGCTACGTGGAGGCGCTGGATGATGAGGAGGAGGAGGAGGAGGAGGAG 855
QY 4975 TATGATGAAGATGCTCAGGTAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGT 5034
Db 856 TATGATGAAGATGCTCAGGTAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGT 915
QY 5035 GAAGAGGAGGAGCTGAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5094
Db 916 GAAGAGGAGGAGCTGAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 975
QY 5095 GTAGATGGCGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAAGAGCGAAAA 5154
Db 976 GTAGATGGCGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAAGAGCGAAAA 1035
QY 5155 TGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5214
Db 1036 CGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1095
QY 5215 TCCTATTGATGTTGACTGTTTACCCATATCCCT-----CCCCCTCCCAATCCTGC 5268
Db 1096 TCCTATTGATGTTGACTGTTTACCCATATCCCTCTCCCCCTCCCAATCCTGC 1155
QY 5269 CCCTGAAACTTACTTTTTCTGATTGAACATGCTGTGGAAATGAGACGGGAAAGTG 5328
Db 1156 CCCTGAAACTTACTTTTTCTGATTGAACATGCTGTGGAAATGAGACGGGAAAGTG 1215

QY 5329 TACTGGGGGTTGTGGAGGAGGGAGGCGAGGAGCGGTGGACTAAATACTATTTTACT 5388
Db 1216 TACTGGGGGTTGCGGGGAGGGATGCGGGTGGGTGGAATAAATACTATTTTACT 1275
QY 5389 GCCAAATAAATAATATTTGTAATATTAATACTGGGATACAGCTTT 5434
Db 1276 GCCACTCTTTATTTTTCCTCCACTTTTCTTTGTCGCGGTTTT 1321

RESULT 11

US-09-699-999-6021
; Sequence 6021, Application US/09699999
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Vasicek, Thomas
; APPLICANT: Wang, Youzhan
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2032-001
; CURRENT APPLICATION NUMBER: US/09/699,999
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,361
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 7488
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6021
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-699-999-6021

Query Match 15.9%; Score 917.6; DB 27; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

QY 4327 TTGGGGCTCGAAGCCAGCGGAGCTGGTTGAGTCTTCAAAGTCCCTAAACGCTGGCGCG 4386
Db 196 TGGGGGCTCGAAGACCAGCGGAGCTGGTTGAGCTTCAAAGTCCCTAAACGCGCGCGCG 255
QY 4387 TGGGTTTCGAGGTTTATGATTGAATTCGGCTGGCAGCAGAGCTCTGCACACAGAGCG 4446
Db 256 TGGGTTTCGAGGTTTATGATTGAATTCGGCGCGCGGAGCTCTGCAGAGAGAGCG 315
QY 4447 CGAGAGATGGAGATGGCGACAGGATTCTATTCAGAGCTGGGGAACAGCGCGCTCTGAT 4506
Db 316 CGAGAGATGGAGATGGCGACAGGATTCTATTCAGAGCTGGGGAACAGCGCGCTCTGAT 375
QY 4507 GTGAAGAACTTGCCTGGCAACAGTCGGTCGATGAATGAAGCAACTCGAAGCCCTCACA 4566
Db 376 GTGAAGAACTTGCCTGGCAACAGTCGGTCGATGAATGAAGCAACTCGAAGCCCTCACA 435
QY 4567 GATGAATTTGAAGAACTTGAATTCCTTAAGTAAATCAACGAGCGCTCACTCAATCTCA 4626
Db 436 GATGAATTTGNAGAACTTGAATTCCTTAAGTAAATCAACGAGCTCACTCAATCTCA 495
QY 4627 GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACTA-----AGAGTCTCAGGG 4674
Db 496 AACTTACCAAGTTTAAACAAACTTAAAGAACTTGAACCTTGAACGATACAGATCTCAGGG 555
QY 4675 GGCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAAC 4734
Db 556 GGCCTGGAAGTATTGGCAGAAAAGTGTCCGAAACCTCAGCATCTATATTTAAGTGGCAAC 615
QY 4735 AAAATTTAAGACCTTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTA 4794
Db 616 AAAATTTAAGACCTTCAGCACAAATAGAGCCACTGAAAGAGTTAGAAAACCTCAAGAGCTTA 675
QY 4795 GACCTTTTCAATTGCGAGGTAACCAACCTGAACGACTTACGGAGAAAACGTTGTTCAAGCTT 4854

Db 676 GACCTTTTCAAATTCGAGGTAAACCACTGAACGACTACCGAGAAATGTGTTCAAGCTC 735
QY 4855 CTCCTGCAACTACATATCTCGACAGCTGTTACTGGGACCAAGAGGAGCCCTTACTCA 4914
Db 736 CTCCTGCAACTACATATCTCGACAGCTGTTACTGGGACCAAGAGGAGCCCTTACTCG 795
QY 4915 GATATTGAGCACACGTCGAGGSCCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGG 4974
Db 796 GATGCTGAGGGCTACGTTGAGGSCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGG 855
QY 4975 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGT 5034
Db 856 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGT 915
QY 5035 GAAGAGGAGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATACGATGAGAG 5094
Db 916 GAAGAGGAGAGCTGAGTGGAGGGGAGGAGGAGGATGAAGAAGGTTATACGATGAGAG 975
QY 5095 GTAGATGGCGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAGGGTCCAGAAGCGAAA 5154
Db 976 GTAGATGACGAGAAGATGAAGAAGCTTGGTGAAGAAGAAGGGTCCAGAAGCGAAA 1035
QY 5155 TGAAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAACCTATTTTGAATAA 5214
Db 1036 CGAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAACCTATTTTGAATAA 1095
QY 5215 TCCTATTGATTGACTGTTTTTACCATATCCCTC-----CCCCCTCCAAATCCTGC 5268
Db 1096 TCCTATTGATTGACTGTTTTTACCATATCCCTC-----CCCCCTCCAAATCCTGC 1155
QY 5269 CCCCAGAACTTACTTTTTCTGATGTAACATGCTGTGGGAATGACGACGGAAGAGTG 5328
Db 1156 CCCCAGAACTTACTTTTTCTGATGTAACGTTGCTGTGGGAACGAGAGGGGAGAGTG 1215
QY 5329 TACTGGGGTGTGGAGGAGGGGAGGAGGAGGCGGTGGACTAAATACTATTTTACT 5388
Db 1216 TACTGGGGTGTGGAGGAGGGAGGATGCGCGGTGGGTGGAATAAATACTATTTTACT 1275
QY 5389 GCCAAATAAATAATATTTGTAATATTAATACTGGGATACAGCTTT 5434
Db 1276 GCCACTCTTTATTTTTCCTCCACTTTTCTTTGTCGCGGTTTT 1321

RESULT 12

US-09-710-281-4371
; Sequence 4371, Application US/09710281
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Stbdal, Hilde
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2036-001
; CURRENT APPLICATION NUMBER: US/09/710,281
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,254
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 5803
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4371
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-710-281-4371

Query Match 15.9%; Score 917.6; DB 28; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

Db	736	CTCCGCAACTACATATCTCGACGGCTATGACCGGACGACAAGGAGGCCCTGACTCG	795
QY	4915	GATATTGAGGACCACTGCGAGGCTTGATGATCAGGAGGAGGCTGACCATGAGGAGG	4974
Db	796	GATCTGAGGCTACGTGCGAGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGG	855
QY	4975	TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGCAGGAGGAGGAGGAAGGT	5034
Db	856	TATGATGAAGATGCTCAGGTAGTGAAGACGAGGAGGAGGATGAGGAGGAGGAAGT	915
QY	5035	GAAGAGGAGGACGTGAGTGGAGGCGACGAGGAGGATGAAGAAGTTTATAACGATGGAG	5094
Db	916	GAAGAGGAGGACGTGAGTGGAGGCGAGGAGGAGGATGAAGAAGTTTATAACGATGGAG	975
QY	5095	GTAGATGCGAGGAAGATGAAGAAGAGCTTGCTGAAGAAGAAAGGCTCAGAAGCGAAA	5154
Db	976	GTAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGCTCAGAAGCGAAA	1035
QY	5155	TGAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAAACCTATTTTGAANAAT	5214
Db	1036	CGAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAAACCTATTTGAANAAT	1095
QY	5215	TCCTATTGTGATTGACTGTTTTTACCCATATCCCTT-----CCGCCCTCCCAATCCTGC	5268
Db	1096	TCCTATTGTGATTGACTGTTTTTACCCATATCCCTTCCCGCCCTCCCAATCCTGC	1155
QY	5269	CCCTGAAACTTACTTTTTTCTGATTGTAACATTCCTGGGAATGAGACGGGAAAAGTG	5328
Db	1156	CCCTGAAACTTATTTTTTCTGATTGTAACCTTGCTGGGAACGAGAGGGGAAGAGTG	1215
QY	5329	TACTGGGGTGTGGAGGAGGAGGAGGAGGCGGTGGACTAAATACATATTTTTTACT	5388
Db	1216	TACTGGGGTGTGGAGGAGGAGGAGGCGGTGGACTAAATACATATTTTTTACT	1275
QY	5389	GCAAAATAAATAATATTGTAATAATTAACCTGGGATAGCTTT 5434	
Db	1276	GCCACTCTTATTTTTTCCCTACTTTTTTCTTGTGTCGGTTTT 1321	
RESULT 14			
US-09-716-973-2254			
; Sequence 2254, Application US/09716973			
; GENERAL INFORMATION:			
; APPLICANT: Shyjan, Andrew W.			
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES			
; TITLE OF INVENTION: THEREFOR			
; FILE REFERENCE: 1600.2042-001			
; CURRENT APPLICATION NUMBER: US/09/716,973			
; CURRENT FILING DATE: 2000-11-21			
; PRIOR APPLICATION NUMBER: 60/167,325			
; PRIOR FILING DATE: 1999-11-24			
; NUMBER OF SEQ ID NOS: 2758			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 2254			
; LENGTH: 1595			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc.feature			
; LOCATION: (1)...(1595)			
; OTHER INFORMATION: n = A,T,C or G			
US-09-716-973-2254			
Query Match 15.9%; Score 917.6; DB 28; Length 1595;			
Best Local Similarity 90.5%; Pred. No. 1.7e-72;			
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;			
QY	4327	TTGGGGCTCGAAGCCGAGCGAGCTGGTTGAGTCTTCAAAGTCTTAAACCTGCGGCCG	4386
Db	196	TGGGGGCTCGAAGCCGAGCGAGCTGGTTGAGCTTCAAAGTCTTAAACCTGCGGCCG	255
QY	4387	TGGGTCGAGGTTTATGATTGAATTCGGCTGCGCAGGAGGCTCTGCGACAGAGCG	4446

Db	256	TGGTTGCGGGTTTATGATTGAATTCGCGCGCGGGAGCCTCTSCAGAGAGAGCG	315
QY	4447	CGAGAGATGAGATGGGCAGACGATTTCATTAGAGCTCGGAACAGGCGCCTCTGAT	4506
Db	316	CGAGAGATGAGATGGGCAGACGATTTCATTAGAGCTCGGAACAGGCGCCTCTGAT	375
QY	4507	GTCAAGAAGACTTCCCTTGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTACA	4566
Db	376	GTCAAGAAGACTTCCCTTGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTACA	435
QY	4567	GATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCTCACCCTCAATCTCA	4626
Db	436	GATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCTCACCCTCAATCTCA	495
QY	4627	GACTTACCACCTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG	4674
Db	496	AACCTTACCACCTTAACCAAACTTAAGAAAGCTTGAACCTAAGCGATAACAGAGCTCAGGG	555
QY	4675	GGCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAAC	4734
Db	556	GGCCTGGAAGTATTGGCAGAAAGTGTCCGAAACCTCACGCATCTAAATTTAAGTGGCAAC	615
QY	4735	AAAAATTAAGACCTCAGCACATAGAGCCACTGAAACAGTTAGAAACCTCAGAGCTTA	4794
Db	616	AAAAATTAAGACCTCAGCACATAGAGCCACTGAAANAGTTAGAAACCTCAGAGCTTA	675
QY	4795	GACCTTTTCAATTCGAGAGTAACCAACCTGAACGACTACGAGAGAAACGTTTCAAGCTT	4854
Db	676	GACCTTTTCAATTCGAGAGTAACCAACCTGAACGACTACGAGAGAAATGTTTCAAGCTC	735
QY	4855	CTCCTGCAACTCACATATCTCAGACGCTGTTACTGGGACCACAGAGGCGCCTTACTCA	4914
Db	736	CTCCCGCAACTCACATATCTCAGACGCTATGACCGGCGACGACAGGAGGCGCCTCAGCTG	795
QY	4915	GATATTGAGGACCACTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGAGGAG	4974
Db	796	GATGCTGAGGGCTACGTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG	855
QY	4975	TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGT	5034
Db	856	TATGATGAAGATGCTCAGGTAGTGAAGACGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGT	915
QY	5035	GAAGAGGAGGACGTGAGTGGAGGCGGACGAGGAGGATGAAGAAGTTTAAACGATGGAGAG	5094
Db	916	GAAGAGGAGGACGTGAGTGGAGGCGGAGGAGGAGGATGAAGAAGTTTAAACGATGGAGAG	975
QY	5095	GTAGATGCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAA	5154
Db	976	GTAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAA	1035
QY	5155	TGAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAAACCTATTTTGAANAAT	5214
Db	1036	CGAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAAACCTATTTTGAANAAT	1095
QY	5215	TCCTATTGTGATTGACTGTTTTTACCCATATCCCTT-----CCGCCCTCCCAATCCTGC	5268
Db	1096	TCCTATTGTGATTGACTGTTTTTACCCATATCCCTTCCCGCCCTCCCAATCCTGC	1155
QY	5269	CCCTGAAACTTACTTTTTTCTGATTGTAACATTCCTGGGAATGAGACGGGAAAAGTG	5328
Db	1156	CCCTGAAACTTATTTTTTCTGATTGTAACCTTGCTGGGAACGAGAGGGGAAGAGTG	1215
QY	5329	TACTGGGGTGTGGAGGAGGAGGAGGAGGCGGTGGACTAAATACATATTTTTTACT	5388
Db	1216	TACTGGGGTGTGGAGGAGGAGGAGGCGGTGGACTAAATACATATTTTTTACT	1275
QY	5389	GCAAAATAAATAATATTGTAATAATTAACCTGGGATAGCTTT 5434	
Db	1276	GCCACTCTTATTTTTTCCCTACTTTTTTCTTGTGTCGGTTTT 1321	
RESULT 15			

US-09-726-172-2050
; Sequence 2050, Application US/09726172
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2052-001
; CURRENT APPLICATION NUMBER: US/09/726.172
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/167,846
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 2733
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2050
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-172-2050

Query Match 15.9%; Score 917.6; DB 29; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;
QY 4327 TTGGGCTCGAGAACCGAGCGAGCTTGGTTGAGTCTTCAAAGTCTCTAAAGCTCGGCGCG 4386
DB 196 TGGGGCTCGAGAACCGAGCGAGCTTGGTTGAGCTTCAAAGCTCGGCGCG 255
QY 4387 TGGGTCGAGGTTTATTGATTTGAATTCGGCTGGCAGGAGGCTTCGACAGACGACG 4446
DB 256 TGGGTTCCGGGTTTATTGATTTGAATTCGCCGCGCGGAGGCTTCGACAGAGAGAGCG 315
QY 4447 CGAGAGATGGAGATGGCAGAGCGGATTCATTCAGAGCTCGGGAACAGGCGCCCTCTGAT 4506
DB 316 CGAGAGATGGAGATGGCAGAGCGGATTCATTCAGAGCTCGGGAACAGGCGCCCTCTGAT 375
QY 4507 GTGAAGAAGACTTGCCTGGACACACAGTCCGATCGAATGAAGGCAAACTGAAGCCCTCACA 4566
DB 376 GTGAAGAAGACTTGCCTGGACACACAGTCCGATCGAATGAAGGCAAACTGAAGCCCTCACA 435
QY 4567 GATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAAGGAGGCTCACCTCAATCTCA 4626
DB 436 GATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAAGTAAATCAAGGCTCACCTCAATCGCA 495
QY 4627 GACTTACCAAGTTA--AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4674
DB 496 AACTTACCAAGTTAACAAGCTTGAAGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 555
QY 4675 GGCTTGAAGTATTGGCAGAAAAGTCTCAAACCTCAGCATCTATATTTAAGTGGCAAC 4734
DB 556 GGCTTGAAGTATTGGCAGAAAAGTCTCAAACCTCAGCATCTATATTTAAGTGGCAAC 615
QY 4735 AAAATTAAGACCTCAGCACAATAGAGCCACTGAACAGCTTAGAAGCTTGAAGACCTCAGAGCTTA 4794
DB 616 AAAATTAAGACCTCAGCACAATAGAGCCACTGAAGAAAGTTAGAAAACCTCAGAGCTTA 675
QY 4795 GACCTTTTCAATTTGCGAGGTAACCAACCTGAACGACTACGGAGAAAACGTTGTCAAGCTT 4854
DB 576 GACCTTTTCAATTTGCGAGGTAACCAACCTGAAGAGCTTACCAGAAATGTGTCAAGCTC 735
QY 4855 CTCTGCAACTCACAATATCTGACAGCTGTTACTGGGACACAGAGGCCCTTACTCA 4914
DB 736 CTCCGCAACTCACAATATCTGACAGCTGTTACTGGGACACAGAGGCCCTTACTCG 795
QY 4915 GATATTGAGGACCCAGGAGGCGCTGGATGACGAGGAGGCTGACATGAGGAGGAG 4974
DB 796 GATGCTGAGGGCTACGTGGAGGGCCCTGGATGATGAGGAGGAGGATGAGGAGGAG 855
QY 4975 TATGATGAAGATGCTCAGGTTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGT 5034

DB 856 TATGATGAAGATGCTCAGGTTAGTGAAGACGAGGAGGAGGATGAGGAGGAGGAGT 915
QY 5035 GAAGAGGAGACGCTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATACGATGGAGAG 5094
DB 916 GAAGAGGAGGACGCTGAGTGGAGGAGGAGGAGGATGAAGAAGGTTATACGATGGAGAG 975
QY 5095 GTAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCAGAAGCGAAAA 5154
DB 976 GTAGATGACGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCAGAAGCGAAAA 1035
QY 5155 TGAGAACCTGAAGATGAGGAGGAGAGATGATGACTAAGTGAATAAACCTATTTTGAAGAAAT 5214
DB 1036 CGAGAACCTGAAGATGAGGAGGAGAGATGATGACTAAGTGAATAAACCTATTTTGAAGAAAT 1095
QY 5215 TCCTATTGCTGATTGACTGTTTTTACCCATATCCCT-----CCCCCTCCCAATCCTGC 5268
DB 1096 TCCTATTGCTGATTGACTGTTTTTACCCATATCCCTCTCCCCCCCCCTCCCAATCCTGC 1155
QY 5269 CCCTGAAACTTACTTTTTCTGATTGTAACATTGCTGGGAATGAGACGGGAAAAAGTG 5328
DB 1156 CCCTGAAACTTACTTTTTCTGATTGTAACATTGCTGGGAACGAGAGGGGGAAGAGTG 1215
QY 5329 TACTGGGGGTTGGAGGAGGAGGAGGAGGCGGTGGACTAAAATACTATTTTACT 5388
DB 1216 TACTGGGGGTTGGGGGAGGAGGATGGGGTGGGGTGGGAATAAAATACTATTTTACT 1275
QY 5389 GCCAAATAAATAATATTTTGAATAATAAATACTGGATAGCTTT 5434
DB 1276 GCCACTCTTTATTTTTCCTTACTTTTTTCTTGTGTCGGGTTTT 1321

Search completed: December 8, 2002, 21:26:38
Job time : 7823 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	5785	100.0	5785	6	US-10-273-334-1	Sequence 1, Appli
2	889	15.4	889	6	US-10-273-334-3	Sequence 3, Appli
3	866.6	15.0	895	6	US-10-273-334-15	Sequence 15, Appl
4	865	15.0	895	6	US-10-273-334-21	Sequence 21, Appl
5	839.4	14.5	895	6	US-10-273-334-23	Sequence 23, Appl
6	831.4	14.4	907	6	US-10-273-334-6	Sequence 6, Appli
7	762.6	13.2	907	6	US-10-273-334-13	Sequence 13, Appl
8	761	13.2	907	6	US-10-273-334-25	Sequence 25, Appl
9	760.2	13.1	906	6	US-10-273-334-33	Sequence 33, Appl
10	757.8	13.1	907	6	US-10-273-334-28	Sequence 28, Appl
11	753	13.0	907	6	US-10-273-334-9	Sequence 9, Appli
12	751.6	13.0	908	6	US-10-273-334-30	Sequence 32, Appl
13	727.4	12.6	907	6	US-10-273-334-32	Sequence 30, Appl
14	716	12.4	905	6	US-10-273-334-4	Sequence 4, Appli
15	711.8	12.3	905	6	US-10-273-334-11	Sequence 11, Appl
16	702	12.1	905	6	US-10-273-334-17	Sequence 17, Appl
17	681.2	11.8	905	6	US-10-273-334-7	Sequence 7, Appli
18	679.6	11.7	905	6	US-10-273-334-19	Sequence 19, Appl
19	679.6	11.7	905	6	US-10-273-334-26	Sequence 26, Appl
20	374.6	6.5	1937	5	US-09-724-676-18913	Sequence 18913, A
21	374.6	6.5	1937	5	US-09-724-676A-18913	Sequence 18913, A
c 22	245.8	4.2	63824	1	PCF-US02-34679-347	Sequence 347, App
c 23	245.8	4.2	63824	1	PCF-US02-34679-348	Sequence 348, App
c 24	245.8	4.2	63824	6	US-10-282-174-347	Sequence 347, App
c 25	245.8	4.2	63824	6	US-10-282-174-348	Sequence 348, App
c 26	245.8	4.2	202100	1	PCF-US02-34679-484	Sequence 484, App

QY 241 CATAAAGTATCTATTTTCATTGAGGAAGAATAAATAGCTACATATTTCTTTTCTTTGTC 300
DB |||||
241 CATAAAGTATCTATTTTCATTGAGGAAGAATAAATAGCTACATATTTCTTTTCTTTGTC 300
QY 301 TTAATATTTGAGGAATTTGCTTATATGTCATAATAAANAAGTTAAAGCCTTATACATTAT 360
DB |||||
301 TTAATATTTGAGGAATTTGCTTATATGTCATAATAAANAAGTTAAAGCCTTATACATTAT 360
QY 361 ACTAAGGAATTTGGACATTAATTTCAAGCTAGCCTTTCTATAAACAANAATGCAATTTTC 420
DB |||||
361 ACTAAGGAATTTGGACATTAATTTCAAGCTAGCCTTTCTATAAACAANAATGCAATTTTC 420
QY 421 TGTCCCTAAATTTGTCCTTCCCTTATTTCCCAATTTCCCAATTTCCCAATTTCCCTCTAG 480
DB |||||
421 TGTCCCTAAATTTGTCCTTCCCTTATTTCCCAATTTCCCAATTTCCCAATTTCCCTCTAG 480
QY 481 CTGCTCAAAACCAAGTACCGGTATGTTATTTCTTAATATATCTTTACCTTGTCTCTCATAT 540
DB |||||
481 CTGCTCAAAACCAAGTACCGGTATGTTATTTCTTAATATATCTTTACCTTGTCTCTCATAT 540
QY 541 GCAATTTGTTAAACAGTATCTTCCAGTCTGTATCCATATTTCTCCCTTTCCAGACCA 600
DB |||||
541 GCAATTTGTTAAACAGTATCTTCCAGTCTGTATCCATATTTCTCCCTTTCCAGACCA 600
QY 601 ACATGCTTTGACTATGCTTACAAATAGCCTCCCAACTCTTTGCTTACTTTAAATTTCA 660
DB |||||
601 ACATGCTTTGACTATGCTTACAAATAGCCTCCCAACTCTTTGCTTACTTTAAATTTCA 660
QY 661 GTAAATAATGACTTTGGCCGGGCAAGTGGCTCACACTATAATTTCCAGACTTTGGGA 720
DB |||||
661 GTAAATAATGACTTTGGCCGGGCAAGTGGCTCACACTATAATTTCCAGACTTTGGGA 720
QY 721 GTCCAGCGGGGGTCCAGAGTCAAGAGTGAAGATGAGACCATCATGCCAACATGSGTAA 780
DB |||||
721 GTCCAGCGGGGGTCCAGAGTCAAGAGTGAAGATGAGACCATCATGCCAACATGSGTAA 780
QY 781 ACCCTGCTCTACTATAATAACAAAAATTTATCTGGGTGTTGGTGGCACATGCTGTAA 840
DB |||||
781 ACCCTGCTCTACTATAATAACAAAAATTTATCTGGGTGTTGGTGGCACATGCTGTAA 840
QY 841 CCCAACTACTAGGAGGCTGAGGAGAGAAATCGCTTGAACCTGGGAGGGAGGTGCA 900
DB |||||
841 CCCAACTACTAGGAGGCTGAGGAGAGAAATCGCTTGAACCTGGGAGGGAGGTGCA 900
QY 901 GTAGCCGAGATCGACATTTGCATCCAGCTGGCAACAGAGGAGACTCCATCCCA 960
DB |||||
901 GTAGCCGAGATCGACATTTGCATCCAGCTGGCAACAGAGGAGACTCCATCCCA 960
QY 961 ACAAAACAAAAACCAATGTAACATGTCGTAAACATGTCAGATTTCTGGTTTCAG 1020
DB |||||
961 ACAAAACAAAAACCAATGTAACATGTCGTAAACATGTCAGATTTCTGGTTTCAG 1020
QY 1021 AAGCTTACATGCTTTTTCATATGCTAAGATAAACCCAAATGCTATTTCTGGTTTCT 1080
DB |||||
1021 AAGCTTACATGCTTTTTCATATGCTAAGATAAACCCAAATGCTATTTCTGGTTTCT 1080
QY 1081 AAAGCCAAAGAAATAAGAGTTCCTTCCAGCAACCTTCTTCTCCGCCATGCTTTTCCCT 1140
DB |||||
1081 AAAGCCAAAGAAATAAGAGTTCCTTCCAGCAACCTTCTTCTCCGCCATGCTTTTCCCT 1140
QY 1141 AGCTCACCTCTTTTGGCAAGTGCACCTGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
DB |||||
1141 AGCTCACCTCTTTTGGCAAGTGCACCTGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
QY 1201 TGGTCTGCTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
DB |||||
1201 TGGTCTGCTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
QY 1261 TTCCTCCCTGGAAATGCTCTCCACTCCAGATGCTTACTAGATCTTTAGCTCAGTCAACCT 1320
DB |||||
1261 TTCCTCCCTGGAAATGCTCTCCACTCCAGATGCTTACTAGATCTTTAGCTCAGTCAACCT 1320

QY 1321 CGCAGGAAGATCTTCCACCATTACCTTCATACACCTATGCTGCTCCCTAGAGAACAT 1380
DB |||||
1321 CGCAGGAAGATCTTCCACCATTACCTTCATACACCTATGCTGCTCCCTAGAGAACAT 1380
QY 1381 CATTCGTTTTTCTTCTACTTCCCTAGCATTACTGCTTCTGAAATATATCTACTTCTGATTC 1440
DB |||||
1381 CATTCGTTTTTCTTCTACTTCCCTAGCATTACTGCTTCTGAAATATATCTACTTCTGATTC 1440
QY 1441 TTATTTCTTTTCTTCTACTTACTAGGATACCTGGGTCATTAAGAGGGGATATTTCTCTC 1500
DB |||||
1441 TTATTTCTTTTCTTCTACTTACTAGGATACCTGGGTCATTAAGAGGGGATATTTCTCTC 1500
QY 1501 TTATTTCTGTTATATAAATTAATGCTTAGGCTGTAAGCTTATACAAATATTTGAGAATA 1560
DB |||||
1501 TTATTTCTGTTATATAAATTAATGCTTAGGCTGTAAGCTTATACAAATATTTGAGAATA 1560
QY 1561 AATCGTTAAATGTATACATTTTGAAGAAAGATAATTTGGGATCCATTTAGTTGCA 1620
DB |||||
1561 AATCGTTAAATGTATACATTTTGAAGAAAGATAATTTGGGATCCATTTAGTTGCA 1620
QY 1621 ACATTTGATCTGTCTTAGACAGAGGCGCATGGTAAAGGACAAAGACATATTTTATAG 1680
DB |||||
1621 ACATTTGATCTGTCTTAGACAGAGGCGCATGGTAAAGGACAAAGACATATTTTATAG 1680
QY 1681 ACTGTACCTGAAAAATAAATAAACTTGAACCATTTATACAAAGCTTATGTCAGGAA 1740
DB |||||
1681 ACTGTACCTGAAAAATAAATAAACTTGAACCATTTATACAAAGCTTATGTCAGGAA 1740
QY 1741 AGGTACCGATTATTTAGAAATGTTAAATCACTTCTAAGCATAACTCAGAGCAATA 1800
DB |||||
1741 AGGTACCGATTATTTAGAAATGTTAAATCACTTCTAAGCATAACTCAGAGCAATA 1800
QY 1801 TATTAGAGGTGAGAGAGAGTGGCTTAGATATTTGTTAATCATATTTAGGACTGAGCG 1860
DB |||||
1801 TATTAGAGGTGAGAGAGAGTGGCTTAGATATTTGTTAATCATATTTAGGACTGAGCG 1860
QY 1861 CATCTTGTATTTTCTTCTGGGAAACAGCTCAAAATGACTATTTAATGTTTACAATGATA 1920
DB |||||
1861 CATCTTGTATTTTCTTCTGGGAAACAGCTCAAAATGACTATTTAATGTTTACAATGATA 1920
QY 1921 TCTTGCATCTGCCAGTAAATATATATAGACACTAGCAATCCAAATGTAAGATGAAC 1980
DB |||||
1921 TCTTGCATCTGCCAGTAAATATATATAGACACTAGCAATCCAAATGTAAGATGAAC 1980
QY 1981 AAGTCTTTTATAGAGGAGAGCCAAATACAAATAACAAAGGTGTAATGCAGTA 2040
DB |||||
1981 AAGTCTTTTATAGAGGAGAGCCAAATACAAATAACAAAGGTGTAATGCAGTA 2040
QY 2041 ATACAAACATACATACCATGTCATAGGAGTGCAGAGAGGTGCTTCTCCGAATGCAGTC 2100
DB |||||
2041 ATACAAACATACATACCATGTCATAGGAGTGCAGAGAGGTGCTTCTCCGAATGCAGTC 2100
QY 2101 ACCCAGAAAGTCTTCTGTAGAAAGGATATCTTAATGGTCTTAAAGGAAAGTAAACC 2160
DB |||||
2101 ACCCAGAAAGTCTTCTGTAGAAAGGATATCTTAATGGTCTTAAAGGAAAGTAAACC 2160
QY 2161 AAAGGCAACTAAAGATTGCAAGAGGTCCCGAGGAAAGCAAAAGCAAAAGGTACATA 2220
DB |||||
2161 AAAGGCAACTAAAGATTGCAAGAGGTCCCGAGGAAAGCAAAAGCAAAAGGTACATA 2220
QY 2221 GGCACAAAAAGTAGCCTGCTTCTTGGGAACTTCCAAATAGTTTCTGGAGCACACAGTTAG 2280
DB |||||
2221 GGCACAAAAAGTAGCCTGCTTCTTGGGAACTTCCAAATAGTTTCTGGAGCACACAGTTAG 2280
QY 2281 AAGTACTGTGCCATGGGACAAAGACTGAAGCATATGAGGTTCAAGGGGCACAGAGCCC 2340
DB |||||
2281 AAGTACTGTGCCATGGGACAAAGACTGAAGCATATGAGGTTCAAGGGGCACAGAGCCC 2340
QY 2341 CATATATGTCATGATAAGATATTGGGAAGCCACTGGGGAGCTACTGAACTTTTAAGCAG 2400
DB |||||
2341 CATATATGTCATGATAAGATATTGGGAAGCCACTGGGGAGCTACTGAACTTTTAAGCAG 2400
QY 2401 GAAATAAAATGTCATATATACACCTTAGAAATTTGATTTTTTCTTCTTTTATCTTTC 2460

[illegible]

Db	3481	TCAGACACAAATTTCTCTAATGCCTGTGCTGCTAACTTCTCAATAGAACACTATATTAATT	3540
QY	3541	TATCTTCTTCCTTGAGTGTGTTTTTCACAAATCCCATAGCCTGTGAAAGATTCGTTTTAGGG	3600
Db	3541	TATCTTCTTCCTTGAGTGTGTTTTTCACAAATCCCATAGCCTGTGAAAGATTCGTTTTAGGG	3600
QY	3601	AAATATTATTTTTAATATAGCATATTTTGTCAATGTGGACATAGACGACTAGTACCTGCTG	3660
Db	3601	AAATATTATTTTTAATATAGCATATTTTGTCAATGTGGACATAGACGACTAGTACCTGCTG	3660
QY	3661	AAACCATCTCATGATCCTTGTTGAAGAACTAATTCACACTAGAAATCTATTTTCCCTTG	3720
Db	3661	AAACCATCTCATGATCCTTGTTGAAGAACTAATTCACACTAGAAATCTATTTTCCCTTG	3720
QY	3721	CTCATTTAAAAACATAAATGCTCTCAGAAAGTAAAAAATTAATTCCTCTCTAATAAACATATC	3780
Db	3721	CTCATTTAAAAACATAAATGCTCTCAGAAAGTAAAAAATTAATTCCTCTCTAATAAACATATC	3780
QY	3781	ATGCCACTCAAAATTTTATTCCTCTACCACTTGGCGTATCTAAACCTAGTTAGATACTTTG	3840
Db	3781	ATGCCACTCAAAATTTTATTCCTCTACCACTTGGCGTATCTAAACCTAGTTAGATACTTTG	3840
QY	3841	GTTTTAGGTATAATCTGACAGAACAGATACAACCAAGATACATTTGTGAGTCAGAAAGTGG	3900
Db	3841	GTTTTAGGTATAATCTGACAGAACAGATACAACCAAGATACATTTGTGAGTCAGAAAGTGG	3900
QY	3901	AAAAATTCATAATTCATGATGATACCAATAAAGATAGATTTAGCTTTTTACAGGATGTTT	3960
Db	3901	AAAAATTCATAATTCATGATGATACCAATAAAGATAGATTTAGCTTTTTACAGGATGTTT	3960
QY	3961	TTGGCATTTTATTCCTTCATTTGAGGGGAGATCTCAACCAAAATATGCTTTTCATGGTTCA	4020
Db	3961	TTGGCATTTTATTCCTTCATTTGAGGGGAGATCTCAACCAAAATATGCTTTTCATGGTTCA	4020
QY	4021	TTGTGTTTATTTAATTTCTGTGATGATATTTCTCAGGTTACTTTAAACCTAGTCTATAGAT	4080
Db	4021	TTGTGTTTATTTAATTTCTGTGATGATATTTCTCAGGTTACTTTAAACCTAGTCTATAGAT	4080
QY	4081	TCAAAGATATCCCGTGTGACGCTCTCAAAAGTAAAAAGAAAAATGGGTACTTTGTGAAGGC	4140
Db	4081	TCAAAGATATCCCGTGTGACGCTCTCAAAAGTAAAAAGAAAAATGGGTACTTTGTGAAGGC	4140
QY	4141	TGATTCACAGTAAGTGTAGAGGGAGTGCCCTGTGTATTCACAAATATATCAACGCTGA	4200
Db	4141	TGATTCACAGTAAGTGTAGAGGGAGTGCCCTGTGTATTCACAAATATATCAACGCTGA	4200
QY	4201	GCATCAGATAGATTTCTTTTAGTCACACACACTTACCTTCTTACTAGAGATCCATAT	4260
Db	4201	GCATCAGATAGATTTCTTTTAGTCACACACACTTACCTTCTTACTAGAGATCCCATAT	4260
QY	4261	ACTTCAATTAATTTCTGCTTTGACCCAGGTTACTTATCAGTCCCTTTATATATATTTG	4320
Db	4261	ACTTCAATTAATTTCTGCTTTGACCCAGGTTACTTATCAGTCCCTTTATATATATTTG	4320
QY	4321	TAAATATTGGGGCTCGAGAACCCAGGCGAGCTGGTTGAGTCTTCAAAGTCCCTAAACGCTG	4380
Db	4321	TAAATATTGGGGCTCGAGAACCCAGGCGAGCTGGTTGAGTCTTCAAAGTCCCTAAACGCTG	4380
QY	4381	CGGCGGTGGGTTGAGGTTTATTTAGTTGAATTCGGCTGGCAGAGAGGCTCTGCAGACAG	4440
Db	4381	CGGCGGTGGGTTGAGGTTTATTTAGTTGAATTCGGCTGGCAGAGAGGCTCTGCAGACAG	4440
QY	4441	AGAGCGCGAGAGATGGAGATGGGCACACGGATTCATTCAGAGCTCGCGAACAGGGCGCCC	4500
Db	4441	AGAGCGCGAGAGATGGAGATGGGCACACGGATTCATTCAGAGCTCGCGAACAGGGCGCCC	4500
QY	4501	TCTGATGTGAAGAACTTGCCTTGGACAAACAGTCCGGTCCGAATGAAGCGCAAACTCGAAGCC	4560
Db	4501	TCTGATGTGAAGAACTTGCCTTGGACAAACAGTCCGGTCCGAATGAAGCGCAAACTCGAAGCC	4560
QY	4561	CTCACAGATGAATTTGAAGAACTGGAAATTCCTTAAGTAAAAATCAACGGAGGCGCTCACTCA	4620
Db	4561	CTCACAGATGAATTTGAAGAACTGGAAATTCCTTAAGTAAAAATCAACGGAGGCGCTCACTCA	4620

QY 4621 ATCTCAGACTTACCAAGTTAAAGCTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGCGCTG 4680
Db 4621 ATCTCAGACTTACCAAGTTAAAGCTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGCGCTG 4680
QY 4681 GAAGTATTGGCAGAAAAGTGCCAAAGCTCACGCGATCTATATTAAAGTGGCAACAAAATT 4740
Db 4681 GAAGTATTGGCAGAAAAGTGCCAAAGCTCACGCGATCTATATTAAAGTGGCAACAAAATT 4740
QY 4741 AAAGACCTCAGACAATAAGAGCCCTACTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTT 4800
Db 4741 AAAGACCTCAGACAATAAGAGCCCTACTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTT 4800
QY 4801 TTCAATTCGGAGGTAAACCACTGAACGACTACGAGAGAAACGTTGTTCAAGCTTCTCCTG 4860
Db 4801 TTCAATTCGGAGGTAAACCACTGAACGACTACGAGAGAAACGTTGTTCAAGCTTCTCCTG 4860
QY 4861 CAACCTCACATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCAGATATT 4920
Db 4861 CAACCTCACATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCAGATATT 4920
QY 4921 GAGGACCACTGGAGGGCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGATGATGAT 4980
Db 4921 GAGGACCACTGGAGGGCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGATGATGAT 4980
QY 4981 GAAGATGCTCAGGTAGTGAAGATCAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5040
Db 4981 GAAGATGCTCAGGTAGTGAAGATCAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5040
QY 5041 GAGGACGTGAGTGGAGGGACGAGGAGGATGAAGAAGTATATAACGATGGAGAGTAGAT 5100
Db 5041 GAGGACGTGAGTGGAGGGACGAGGAGGATGAAGAAGTATATAACGATGGAGAGTAGAT 5100
QY 5101 GCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAAGAGGGGTGAGAGCGAAATGAGAA 5160
Db 5101 GCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAAGAGGGGTGAGAGCGAAATGAGAA 5160
QY 5161 CTTGAAGATGAGGAGAAAGATGATGACTAAGTGAATAACCTATTTTGAAGAAATTCCTAT 5220
Db 5161 CTTGAAGATGAGGAGAAAGATGATGACTAAGTGAATAACCTATTTTGAAGAAATTCCTAT 5220
QY 5221 TGTGATTTGACTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 5280
Db 5221 TGTGATTTGACTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 5280
QY 5281 ACTTTTCTGATGTAACATTCGCTGGGAATGAGCGGGAAGAGTGACTGGGGGTG 5340
Db 5281 ACTTTTCTGATGTAACATTCGCTGGGAATGAGCGGGAAGAGTGACTGGGGGTG 5340
QY 5341 TGGAGGAGGAGGAGGAGGAGGCGGTGGACTAAAATGACTATTTTACTGCCAAATATAAT 5400
Db 5341 TGGAGGAGGAGGAGGAGGAGGCGGTGGACTAAAATGACTATTTTACTGCCAAATATAAT 5400
QY 5401 AATATTTGTAATATTAACCTGGGATGACTAGCTTTGTAGATGATTAATTTATTTCT 5460
Db 5401 AATATTTGTAATATTAACCTGGGATGACTAGCTTTGTAGATGATTAATTTATTTCT 5460
QY 5461 CTCTCTTTTATTTTATACACTTCTATCTTTTAAAGTATAGTCCCTTTAGTCCCAAG 5520
Db 5461 CTCTCTTTTATTTTATACACTTCTATCTTTTAAAGTATAGTCCCTTTAGTCCCAAG 5520
QY 5521 GAAAAGGCACTACAATCCACTTATTAATGCTTGCTACTGTGTGCTCAAGTAAAATAGCTCC 5580
Db 5521 GAAAAGGCACTACAATCCACTTATTAATGCTTGCTACTGTGTGCTCAAGTAAAATAGCTCC 5580
QY 5581 AGGATTTAACAAAAGAGGAGAAAGAAATATTTACATGAAATGTTGCTTAAAGTTTAA 5640
Db 5581 AGGATTTAACAAAAGAGGAGAAAGAAATATTTACATGAAATGTTGCTTAAAGTTTAA 5640
QY 5641 ACAAATTCAGTAAATGATTTGTTAAAGCAAAATTCCTATTTTAAATTTTAAATTAAGA 5700
Db 5641 ACAAATTCAGTAAATGATTTGTTAAAGCAAAATTCCTATTTTAAATTTTAAATTAAGA 5700

QY 5701 AATAATTTCTAAAGCAAAATTTTGGAAAAATAAATGACACTTTTACTTGATTTTATT 5760
Db 5701 AATAATTTCTAAAGCAAAATTTTGGAAAAATAAATGACACTTTTACTTGATTTTATT 5760
QY 5761 TATTAACAAATCATTTAAGCTT 5785
Db 5761 TATTAACAAATCATTTAAGCTT 5785
RESULT 2
US-10-273-334-3
; Sequence 3, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-3
Query Match 15.4%; Score 889; DB 6; Length 889;
Best Local Similarity 100.0%; Pred. No. 4.6e-86;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4388 GGGTTTCGAGGTTTATTGATTGAATTCGGCTGGCACAGAGCCCTCTGCAGACAGAGAGCGC 4447
Db 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCACAGAGAGCCCTCTGCAGACAGAGAGCGC 60
QY 4448 GAGAGATGGAGATGGGAGAGCGGATTCATTTCAGAGCTCGGGAACAGAGCGCCCTCTGATG 4507
Db 61 GAGAGATGGAGATGGGAGAGCGGATTCATTTCAGAGCTCGGGAACAGAGCGCCCTCTGATG 120
QY 4508 TGAAGAACTTGCCCTCGCAACAGTCGGTCTGAATGAAGGCAAACTCGAAGCCCTTCACAG 4567
Db 121 TGAAGAACTTGCCCTCGCAACAGTCGGTCTGAATGAAGGCAAACTCGAAGCCCTTCACAG 180
QY 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 4627
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240
QY 4628 ACTTACCAGAACTTAAAGTTGAGAAGCTTGAACCTAAGAGTCTCAGGGGCTCGAAGTAT 4687
Db 241 ACTTACCAGAACTTAAAGTTGAGAAGCTTGAACCTAAGAGTCTCAGGGGCTCGAAGTAT 300
QY 4688 TGGCAAGAAAGTGTCCTCAAACTCACGATCTATATTTAAAGTGGCAACAAATTAAGACCC 4747
Db 301 TGGCAAGAAAGTGTCCTCAAACTCACGATCTATATTTAAAGTGGCAACAAATTAAGACCC 360
QY 4748 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 4807
Db 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
QY 4808 GCGAGGTAAACCACTGAACGACTACGGAGAAACGCTTCTCAAGCTTCTCTGCAACTCA 4867
Db 421 GCGAGGTAAACCACTGAACGACTACGGAGAAACGCTTCTCAAGCTTCTCTGCAACTCA 480
QY 4868 CATATCTCGACAGCTGTTTACTGGGACCACAGGAGGCCCTTACTCAGATATTGAGGACC 4927
Db CATATCTCGACAGCTGTTTACTGGGACCACAGGAGGCCCTTACTCAGATATTGAGGACC 4927

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Db 481 CATATCTCGACAGCTGTTACTGGGACCACAAGAGGCGCCCTTACTCAGATATTGAGGACC 540
QY 4928 ACGTGGAGGCGCTGATACACGAGGAGGAGGTGAGCATGAGGAGGATGATGATGAAAGATG 4997
Db 541 ACGTGGAGGCGCTGATGACGAGGAGGAGGAGGTGAGCATGAGGAGGATGATGATGAAAGATG 600
QY 4988 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Db 601 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 5048 TGAGTGGAGGCGGAGGAGGATGAAGAAGGTTATACAGATGAGAGAGGTAGATGGCGAGG 5107
Db 661 TGAGTGGAGGCGGAGGAGGATGAAGAAGGTTATACAGATGAGAGAGGTAGATGGCGAGG 720
QY 5108 AAGATGAAGAAGAGCTTGCTGAACAAGAAAGGGCTCAGACCGGAAATGAGAACCTGAAG 5167
Db 721 AAGATGAAGAAGAGCTTGCTGAACAAGAAAGGGCTCAGACCGGAAATGAGAACCTGAAG 780
QY 5168 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 5227
Db 781 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 840
QY 5228 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 5276
Db 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 889

RESULT 3
US-10-273-334-15
; Sequence 15, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-10-273-334-15

Query Match 15.0%; Score 866.6; DB 6; Length 895;
Best Local Similarity 98.9%; Pred. No. le-83;
Matches 885; Conservative 0; Mismatches 4; Indels 6; Gaps 1;

QY 4388 GGGTTCGAGGTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTCGACAGAGAGCGC 4447
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTCGACAGAGAGCGC 60
QY 4448 GAGAGATGAGATGGGCGACAGCGATTCAATCAGAGCTGGGAAACAGGGCGCCCTCTGATG 4507
Db 61 GAGAGATGAGATGGGCGACAGCGATTCAATCAGAGCTGGGAAACAGGGCGCCCTCTGATG 120
QY 4508 TGAAGAAGACTTGCCTGGACAAACAGTCGGTCGAATGAAGCGAAACCTCGAAGCCCTCACAG 4567
Db 121 TGAAGAAGACTTGCCTGGACAAACAGTCGGTCGAATGAAGCGAAACCTCGAAGCCCTCACAG 180
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QY 4568 ATCAATTTGAGAACTGGAAATCTTAAAGTAAATCAACGAGGCGCCTCACTCAATCTCAG 4627
Db 181 ATCAATTTGAGAACTGGAAATCTTAAAGTAAATCAACGAGGCGCCTCACTCAATCTCAG 240
QY 4628 ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAACATAAGAGTCTCAGGGGCGCTTGAAGATAT 4687
Db 241 ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAACATAAGAGTCTCAGGGGCGCTTGAAGATAT 300
QY 4688 TGCGAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAAGTGGCAACAAAATTAAGAGACC 4747
Db 301 TGCGAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAAGTGGCAACAAAATTAAGAGACC 360
QY 4748 TCAGCACAAATAGAGCCACCTGAACACAGTTAGAAAACCTCAAGAGCTTAGACCTTTCAATT 4807
Db 361 TCAGCACAAATAGAGCCACCTGAACACAGTTAGAAAACCTCAAGAGCTTAGACCTTTCAATT 420
QY 4808 GCGAGGTAACCAACCTTGAACGACTACGGAGAAAACCTGTTCAAGCTTCTCCCTGCAACTCA 4867
Db 421 GCGAGGTAACCAACCTTGAACGACTACGGAGAAAACCTGTTCAAGCTTCTCCCTGCAACTCA 480
QY 4868 CATATCTCGACAGCTGTTACTGGGACCACAAGAGGCGCCCTTACTCAGATATTGAGGACC 4927
Db 481 CATATCTCGACAGCTGTTACTGGGACCACAAGAGGCGCCCTTACTCAGATATTGAGGACC 540
QY 4928 ACGTGGAGGCGCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGATGATGATGAAAGATG 4987
Db 541 ACGTGGAGGCGCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGATGATGATGAAAGATG 600
QY 4988 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Db 601 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 5048 TGAGTGGAGGCGGACGAGGAGGATGAAGAAGTTATAACGATGGAGAGGTAGATGGCGAGG 5107
Db 661 TGAGTGGAGGCGGACGAGGAGGATGAAGAAGTTATAACGATGGAGAGGTAGATGGCGAGG 720
QY 5108 AGATGAACAAGAGCTTGTGTAAGAAGAAGGGTTCAGAACGAAATGAGAACCTGAAG 5167
Db 721 AAGATGAAGAAGAGCTTGTGTAAGAAGAAGGGTTCAGAACGAAATGAGAACCTGAAG 780
QY 5168 ATGAGGAGAGAAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 5227
Db 781 ATGAGGAGAGAAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 840
QY 5228 TGACTGTTTTTACCATATC-----CCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 5276
Db 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 895
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RESULT 4
US-10-273-334-21
; Sequence 21, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-10-273-334-21

Query Match      15.0%; Score 865; DB 6; Length 895;
Best Local Similarity 98.8%; Pred. No. 1.5e-83;
Matches 884; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGCCACGAGAGCCTCTGCAGACGAGAGCGC 4447
Db      1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGCCACGAGAGCCTCTGCAGACGAGAGCGC 60

Qy 4448 GAGAGATGAGATGGCAGACGGATTTCATTTCAGAGCTCGGAAACAGGCGGCCCTCTGATG 4507
Db      61 GAGAGATGAGATGGCAGACGGATTTCATTTCAGAGCTCGGAAACAGGCGGCCCTCTGATG 120

Qy 4508 TGAAGAAGACTTCCCTCGGACACAGCTCGGTGGAATGAAGGCAAACTCGAAGCCCTTCACAG 4567
Db      121 TGAAGAAGACTTCCCTCGGACACAGCTCGGTGGAATGAAGGCAAACTCGAAGCCCTTCACAG 180

Qy 4568 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG 4627
Db      181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG 240

Qy 4628 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGCCCTGGAAGTAT 4687
Db      241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGCCCTGGAAGTAT 300

Qy 4688 TGGCAGAAAGTGTCCAAACCTCAGCAGCTGAACTGAAAGCTTAGACCTTTTCAATT 4807
Db      301 TGGCAGAAAGTGTCCAAACCTCAGCAGCTGAACTGAAAGCTTAGACCTTTTCAATT 420

Qy 4808 GCAGGTAAACCAACCTGAACGACTACGGAGAAAGCTGTTCAAGCTTCTCCTGCAACTCA 4867
Db      421 GCAGGTAAACCAACCTGAACGACTACGGAGAAAGCTGTTCAAGCTTCTCCTGCAACTCA 480

Qy 4868 CATATCTGACAGCTGTTTACTGGGACCAAGAGAGGCCCTTACTCAGATATGAGGACC 4927
Db      481 CATATCTGACAGCTGTTTACTGGGACCAAGAGAGGCCCTTACTCAGATATGAGGACC 540

Qy 4928 ACCTGAGGGCCTGGATGACGAGGAGGGTGCAGATGAGGAGGCTTACTCAGATATGAGGATG 4987
Db      541 ACCTGAGGGCCTGGATGACGAGGAGGGTGCAGATGAGGAGGCTTACTCAGATATGAGGATG 600

Qy 4988 CTCAGGTAGTGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Db      601 CTCAGGTAGTGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660

Qy 5048 TGAGTGGAGGGACGAGGAGGATGAAGAAGTTATACGATGAGAGGTAGATGGCGAGG 5107
Db      661 TGAGTGGAGGGACGAGGAGGATGAAGAAGTTATACGATGAGAGGTAGATGGCGAGG 720

Qy 5108 AAGATGAAGAGAGCTTGGTGRAGAGAGAGGGGTGAGAGCGGAAATCAGAACCTGGAAG 5167
Db      721 AAGATGAAGAGAGCTTGGTGRAGAGAGAGGGGTGAGAGCGGAAATCAGAACCTGGAAG 780

Qy 5168 ATGAGGAGAGATGATGACTAGTGAATAACCTATTTTGAAGAAATTCCTATTGTGATT 5227
Db      781 ATGAGGAGAGATGATGACTAGTGAATAACCTATTTTGAAGAAATTCCTATTGTGATT 840

Qy 5228 TGACTGTTTTACCCATATC-----CCCTCCCCCTCCCAATCCTGCCCCCTGAA 5276
Db      841 TGACTGTTTTACCCATATC-----CCCTCCCCCTCCCAATCCTGCCCCCTGAA 895

RESULT 5
US-10-273-334-23

; Sequence 23, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: patentin version 3.1
; SEQ ID NO 23
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-10-273-334-23

Query Match      14.5%; Score 839.4; DB 6; Length 895;
Best Local Similarity 97.0%; Pred. No. 7.3e-81;
Matches 868; Conservative 0; Mismatches 21; Indels- 6; Gaps 1;

Qy 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACGAGAGCGC 4447
Db      1 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGCGGAGCCTCTGCAGAGAGGAGCGC 60

Qy 4448 GAGAGATGAGATGGGAGAGCGGATTTCATTTCAGAGCTGCGGAACAGAGGCCCTCTGATG 4507
Db      61 GAGAGATGAGATGGGAGAGCGGATTTCATTTCAGAGCTGCGGAACAGAGGCCCTCTGATG 120

Qy 4508 TGAAGAAGCTTGCCTCGCACAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 4567
Db      121 TGAAGAAGCTTGCCTCGCACAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 180

Qy 4568 ATGAATTTGAAGAAGCTGGAATTCCTTAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG 4627
Db      181 ATGAATTTGAAGAAGCTGGAATTCCTTAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG 240

Qy 4628 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGCCCTGGAAGTAT 4687
Db      241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGCCCTGGAAGTAT 300

Qy 4688 TGGCAGAAAGTGTCCAAACCTCAGCAGCTGAACTGAAAGCTTAGACCTTTTCAATT 4747
Db      301 TGGCAGAAAGTGTCCAAACCTCAGCAGCTGAACTGAAAGCTTAGACCTTTTCAATT 420

Qy 4808 GCAGGTAAACCAACCTGAACGACTACGGAGAAAGCTGTTCAAGCTTCTCCTGCAACTCA 4867
Db      421 GCAGGTAAACCAACCTGAACGACTACGGAGAAAGCTGTTCAAGCTTCTCCTGCAACTCA 480

Qy 4868 CATATCTGACAGCTGTTTACTGGGACCAAGAGAGGCCCTTACTCAGATATGAGGACC 4927
Db      481 CATATCTGACAGCTGTTTACTGGGACCAAGAGAGGCCCTTACTCAGATATGAGGACC 540

Qy 4928 ACCTGAGGGCCTGGATGACGAGGAGGGTGCAGATGAGGAGGCTTACTCAGATATGAGGATG 4987
Db      541 ACCTGAGGGCCTGGATGACGAGGAGGGTGCAGATGAGGAGGCTTACTCAGATATGAGGATG 600

Qy 4988 CTCAGGTAGTGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Db      601 CTCAGGTAGTGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660

Qy 5048 TGAGTGGAGGGACGAGGAGGATGAAGAAGTTATACGATGAGAGGTAGATGGCGAGG 5107
Db      661 TGAGTGGAGGGACGAGGAGGATGAAGAAGTTATACGATGAGAGGTAGATGGCGAGG 720

Qy 5108 AAGATGAAGAGAGCTTGGTGRAGAGAGAGGGGTGAGAGCGGAAATCAGAACCTGGAAG 5167
Db      721 AAGATGAAGAGAGCTTGGTGRAGAGAGAGGGGTGAGAGCGGAAATCAGAACCTGGAAG 780

Qy 5168 ATGAGGAGAGATGATGACTAGTGAATAACCTATTTTGAAGAAATTCCTATTGTGATT 5227
Db      781 ATGAGGAGAGATGATGACTAGTGAATAACCTATTTTGAAGAAATTCCTATTGTGATT 840

Qy 5228 TGACTGTTTTACCCATATC-----CCCTCCCCCTCCCAATCCTGCCCCCTGAA 5276
Db      841 TGACTGTTTTACCCATATC-----CCCTCCCCCTCCCAATCCTGCCCCCTGAA 895

RESULT 5
US-10-273-334-23
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Best Local Similarity 92.6%; Pred. No. 8.3e-73;					
Matches 840; Conservative 0; Mismatches 49; Indels 18; Gaps 3;					
<hr/>					
Qy	4388	GGGTTTCGAGGTATTAATTGAATTCGGCTGGCACGAGAGCCTTCTCGACAGACAGAGCC 4447			
Db	1	GGGTTCGGGGTTTTATGATGATGAAATTCGCCCGCGCGGAGCCCTCTCGAGAGAGAGCCG 60			
<hr/>					
Qy	4448	GAGAGATGAGATGGGCACAGCGGATTCATTACAGAGCTCGGAAACAGGGGCGCCTCTGATG 4507			
Db	61	GAGAGATGAGATGGGCACAGCGGATTCATTAGAGCTGCGGAAACAGAGCGCCCTCTGATG 120			
<hr/>					
Qy	4508	TGAAAGAAGCTTGCCCTGGACAACAGTCGGTTCGAATGAAGCGAAGCTTCGAAGCCCTCACAG 4567			
Db	121	TGAAAGAAGCTTGTCTCTGGACACACAGTCGGTTCGAATGAAGCGAAGCTTCGAAGCCCTCACAG 180			
<hr/>					
Qy	4568	ATCAATTTGAAGAAGCTTGAATTTCTTAAGTATAAATCAACGGAGGCGCTCACCTCAATCTCAG 4627			
Db	181	ATGAATTTGAAGAAGCTTGAATTTCTTAAGTACAACTCAACGTAGGCGCTACCCTCAATCGCAA 240			
<hr/>					
Qy	4628	ACTATCAAAAGTTA---AAGTTTGAAAAGCTTTGAAGT-----AGAGTCTCAGGG 4675			
Db	241	ACTTACCAAGTTTAAACAACTTAAAGAGCTTGAACCTAAGCGATAACAGAGTCTCAGGG 300			
<hr/>					
Qy	4676	GCCCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTTCAGCGATCTATATTAAATGCGCAACA 4735			
Db	301	GCCCTGGAAGTATTGGCAGAAAAAGTGTCCGAAACCTTCAGCGATCTAAATTTAAGTGGCAACA 360			
<hr/>					
Qy	4736	AAMATTAAAGACCTTCAGCACAAATAGAGCCACCTGAACAGTTAGAAAACCTTCAGAGCTTAG 4795			
Db	361	AAMATTAAAGACCTTCAGCACAAATAGAGCCACCTGA AAAAAGCTTAGAAAACCTTCAGAGCTTAG 420			
<hr/>					
Qy	4796	ACCTTTTCAATTTGCGAGGTGAACCAACCTTGAACGACTACGGAGAAAAGCTGTTCAAGCTTC 4855			
Db	421	ACCTTTTCAATTTGCGAGGTGAACCAACCTTGAACGACTACCGAGAAAATGTTTCAAGCTCC 480			
<hr/>					
Qy	4856	TCCTGCAACTTCACATATCTCGACAGCTTTACTGGGACCAAGAGGAGGCCCTTACTCTAG 4915			
Db	481	TCCCGCAACTTCACATATCTCGACGGCTATGACCGGGACGACAAGGAGGCCCTGACTCGG 540			
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Qy	4916	ATATTGAGGACCCTGGAGGGCCCTGGATGACGAGGAGGAGGGGTGACCATGAGGAGAGGT 4975			
Db	541	ATGCTGAGGGCTACGTTGGAGGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 600			
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Qy	4976	ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGGAAGGTG 5035			
Db	601	ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGAGGAGGAGGATGAGGAGGAGGAAGT 660			
<hr/>					
Qy	5036	AAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGTAAGAAGGTTATPACGATGGAGAG 5095			
Db	661	AAGAGGAGGACGTGAGTGGAGAGGAGGAGGAGGATGAAGAAGGTTATPACGATGGAGAGG 720			
<hr/>					
Qy	5096	TGATGCGGAGGAAGATGAAGAAGCTTGGTGAAGAGAAAGGGGTCAACAAGCAAAAT 5155			
Db	721	TGATGACGAGGAAGATGAAGAAGCTTGGTGAAGAGAAAGGGGTCAAGAAGCAAAAC 780			
<hr/>					
Qy	5156	GAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAAATACCTATATTTTGAAAAAT 5215			
Db	781	GAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAAATACCTATATTTTGAAAAAT 840			
<hr/>					
Qy	5216	CCATATGTGATTTGACTGTTTTTACCACATATCCCCCT-----CCCCCCTCCAATCTCTGCC 5269			
Db	841	CCTATTGTGATTTGACTGTTTTTACCACATATCCCCCTTCCCCCCCCCCTCTAATCTCTGCC 900			
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Qy	5270	CCCTGAA 5276 			
Db	901	CCCTGAA 907 			
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RESULT 8					
US-10-273-334-25					
; Sequence 25, Application US/10273334					
; GENERAL INFORMATION:					
; APPLICANT: Pasternack, Gary R.					


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Query Match      13.1%; Score 757.8; DB 6; Length 907;
Best Local Similarity 92.3%; Pred. No. 2.6e-72;
Matches 837; Conservative 0; Mismatches 52; Indels 18; Gaps 3;

QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGGAGAGCCTCTGCAGACAGAGAGCGC 4447
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGCCGGCGGGAGGCTCTGCAGAGAGAGAGCGC 60

QY 4448 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGGAAACAGGGCGCCCTCTGATG 4507
Db 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGGAAACAGGGCGCCCTCTGATG 120

QY 4508 TGAAGAAGCTTCCCTCGCACACAGTCGCTGAATGAAGGCAAACTCGAAGCCCTCACAG 4567
Db 121 TGAAGAAGCTTCTCTCGTTCACAGTCGCTGAATGAAGGCAAACTCGAAGCCCTCACAG 180

QY 4568 ATGAATTTGAAGAAGCTGGAATTTAAGTAAATCAACGGAGGCGCTCACTCAATCTCAG 4627
Db 181 ATGAATTTGAAGAAGCTGGAATTTAAGTAAATCAACGGAGGCGCTCACTCAATCGCAA 240

QY 4628 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 4675
Db 241 ACTTACCAAGTTAACAACCTTAAGAAGCTTGAAGCTAAGCGATAACAGAGTCTCAGGGG 300

QY 4676 GCGTGGAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACA 4735
Db 301 GCGTGAAGTATTGGCAGAAAAAGTGTCCGAACCTCACGCATCTAAATTTAAGTGGCAACA 360

QY 4736 AAATTAAGACCTCAGCACAATAGAGCCNCTGAAACAGATTAGAAAACTCAAGAGCTTAG 4795
Db 361 AAATTAAGACCTCAGCACAATAGAGCCNCTGAAAGAGTTAGAAAACTCAAGAGCTTAG 420

QY 4796 ACCTTTTCAATTCGAGGTAACCAACCTGAACGACTACGGAGAGAAACCTGTTCAGGCTC 4855
Db 421 ACCTTTTCAATTCGAGGTAACCAACCTGAACGACTACGGAGAGAAATGTGTTCAGGCTC 480

QY 4856 TCCGTGCAACTCACATATCTCGACAGCTGTACTGGGACCAACAGGAGGCCCTTACTCAG 4915
Db 481 TCCGTGCAACTCACATATCTCGACGCTGTATGACCGGGACGACAAAGGAGGCCCTGACTCGG 540

QY 4916 ATATTGAGGACCTGGAGGCGCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGT 4975
Db 541 ATGCTGAGGCGCTACGTGGAGGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 600

QY 4976 ATGATGAAGATGCTCAGGTAGTGAAGATGAGAGGGCGGAGGAGGAGGAGGAGGAGT 5035
Db 601 ATGATGAAGATGCTCAGGTAGTGAAGATGAGAGGGCGGAGGAGGAGGAGGAGGAGT 660

QY 5036 AAGAGGAGGAGCTGAGTGGAGGGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG 5095
Db 661 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG 720

QY 5096 TAGATCGCAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAT 5155
Db 721 TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAC 780

QY 5156 GAGAAGCTGAAGATGAGGAGAGAGATGATGACTTAAGTAGAATAAAGCTATTTTGAAGAAAT 5215
Db 781 GAGAAGCTGAAGATGAGGAGAGAGATGATGACTTAAGTGAATAAAGCTATTTTGAAGAAAT 840

QY 5216 CCTATTGTGATTTGACTGTTTTTACCATAATCCCT- - - - -CCCCCTCCAAATCCTGCC 5269
Db 841 CCTATTGTGATTTGACTGTTTTTACCATAATCCCTTCTCCCTCCCTCCCTCTTAATCCTGCC 900

QY 5270 CCCTGAA 5276
Db 901 CCCTGAA 907
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RESULT 11
US-10-273-334-9
; Sequence 9, Application US/10273334
; GENERAL INFORMATION:

```
; APPLICANT: Pasternack, Gary R.  
; APPLICANT: Kochevar, Gerald J.  
; APPLICANT: Brody, Jonathan R.  
; APPLICANT: Kodkol, Shihari S.  
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY  
; FILE REFERENCE: 031787.0076  
; CURRENT APPLICATION NUMBER: US/10/273,334  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: US/09/591,500  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: PCT/US98/26433  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: US 60/069,677  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 907  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (66)..(812)  
; OTHER INFORMATION:  
; US-10-273-334-9
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Query Match 13.0%; Score 753; DB 6; Length 907;
Best Local Similarity 92.0%; Pred. No. 8.4e-72;
Matches 834; Conservative 0; Mismatches 55; Indels 18; Gaps 3;

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QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGGAGCCTCTGCAGACAGAGAGCGC 4447
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGCCGGCGGGAGGCTCTGCAGAGAGAGAGCGC 60

QY 4448 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGGAAACAGGGCGCCCTCTGATG 4507
Db 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGGAAACAGGGCGCCCTCTGATG 120

QY 4508 TGAAGAAGCTTCCCTCGCACACAGTCGCTGAATGAAGGCAAACTCGAAGCCCTCACAG 4567
Db 121 TGAAGAAGCTTGTCTCGACAAACAGTCGCTGAATGAAGGCAAACTCGAAGCCCTCACAG 180

QY 4568 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAG 4627
Db 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCGCAA 240

QY 4628 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 4675
Db 241 ACTTACCAAGTTAACAACCTTAAAGAAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG 300

QY 4676 GCGTGGAGATTTGGCAGAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGCAACA 4735
Db 301 GCGTGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGCAACA 360

QY 4736 AAATTAAGACCTCAGCACAATAGAGCCNCTGAAACAGTTAGAAAACTCAAGAGCTTAG 4795
Db 361 AAATTAAGACCTCAGCACAATAGAGCCNCTGAAAGAGTTAGAAAACTCAAGAGCTTAG 420

QY 4796 ACCTTTTCAATTCGAGGTAACCAACCTGAACGACTACGGAGAGAAACCTGTTCAGGCTC 4855
Db 421 ACCTTTTCAATTCGAGGTAACCAACCTGAACGACTACGGAGAGAAATGTGTTCAGGCTC 480

QY 4856 TCCGTGCAACTCACATATCTCGACAGCTGTACTGGGACCAACAGGAGGCCCTTACTCAG 4915
Db 481 TCCGTGCAACTCACATATCTCGACGCTGTATGACCGGGACGACAAAGGAGGCCCTGACTCGG 540

QY 4916 ATATTGAGGACCTGGAGGCGCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGT 4975
Db 541 ATGCTGAGGCGCTACGTGGAGGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 600

QY 4976 ATGATGAAGATGCTCAGGTAGTGAAGATGAGAGGGCGGAGGAGGAGGAGGAGGAGT 5035
Db 601 ATGATGAAGATGCTCAGGTAGTGAAGATGAGAGGGCGGAGGAGGAGGAGGAGGAGT 660

QY 5036 AAGAGGAGGAGCTGAGTGGAGGGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG 5095
Db 661 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG 720

QY 5096 TAGATCGCAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAT 5155
Db 721 TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAC 780

QY 5156 GAGAAGCTGAAGATGAGGAGAGAGATGATGACTTAAGTAGAATAAAGCTATTTTGAAGAAAT 5215
Db 781 GAGAAGCTGAAGATGAGGAGAGAGATGATGACTTAAGTGAATAAAGCTATTTTGAAGAAAT 840

QY 5216 CCTATTGTGATTTGACTGTTTTTACCATAATCCCT- - - - -CCCCCTCCAAATCCTGCC 5269
Db 841 CCTATTGTGATTTGACTGTTTTTACCATAATCCCTTCTCCCTCCCTCCCTCTTAATCCTGCC 900

QY 5270 CCCTGAA 5276
Db 901 CCCTGAA 907
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QY 5036 AAGAGGAGAGCTGAGTGGAGGGACGAGGAGGATGAAGAAGCTTATAACGATGAGAGG 5095
|||||
Db 661 AAGAGGAGAGCTGAGTGGAGGAGGAGGAGGATGAAGAAGCTTATAACGATGAGAGG 720
|||||
QY 5096 TAGATGGCGAGAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAT 5155
|||||
Db 721 TAGATGAGGAGAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAT 780
|||||
QY 5156 GAGAACCTGAAGATGAGGAGGAGAGATGACTAAGTAGAATAACCTATTGAAAAAT 5215
|||||
Db 781 GAGAACCTGAAGATGAGGAGGAGAGATGACTAAGTAGAATAACCTATTGAAAAAT 840
|||||
QY 5216 CCTATTGATTTGACTGTTTTTACCCTATCCCT-----CCCCCTCCAACTCTGCC 5269
|||||
Db 841 CCTATTGATTTGACTGTTTTTACCCTATCCCTCTCCCCCTCTAATCCTGCC 900
|||||
QY 5270 CCCTGAA 5276
|||||
Db 901 CCCTGAA 907
|||||
RESULT 12
US-10-273-334-32
; Sequence 32, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-32

Query Match 13.0%; Score 751.6; DB 6; Length 908;
Best Local Similarity 92.5%; Pred. No. 1.2e-71;
Matches 840; Conservative 0; Mismatches 49; Indels 19; Gaps 4;

QY 4388 GGGTTCGAGCTTATTGATTCGCTGGCTGGACGAGGCTCTGACAGAGAGCGC 4447
|||||
Db 1 GGGTTCGAGCTTATTGATTCGCTGGCTGGACGAGGCTCTGACAGAGAGAGCGC 60
|||||
QY 4448 -GAGAGATGAGATGGGACAGGATTCATTGAGAGCTGGGAAACAGGGCGCTCTGAT 4506
|||||
Db 61 GGAGAGATGAGATGGGACAGGATTCATTGAGAGCTGGGAAACAGGGCGCTCTGAT 120
|||||
QY 4507 GTGAAGAATCTGCCCTGGACACAGTCGCTCGAATGAAGGAACTCGAAGCCCTACA 4566
|||||
Db 121 GTGAAGAATCTGCCCTGGACACAGTCGCTCGAATGAAGGAACTCGAAGCCCTACA 180
|||||
QY 4567 GATGAATTCGAAGCTGGAATCTTAAGTAAATCAACGGAGGCTACCTCAATCTCA 4626
|||||
Db 181 GATGAATTCGAAGCTGGAATCTTAAGTAAATCAACGGAGGCTACCTCAATCTCA 240
|||||
QY 4627 GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGG 4674
|||||
Db 241 AACTTACCAAGTTAACAACCTTAGAAGCTTAGAGCTTAGCGATACAGAGTCTCAGG 300
|||||
QY 4675 GGCTTGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTAAAGTGGCAAC 4734
|||||

Db 301 GGCTTGAAGTATTGGCAGAAAAAGTGTCCGAACCTCACGCATCTAAATTTAAGTGGCAAC 360
|||||
QY 4735 AAAATTTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTA 4794
|||||
Db 361 AAAATTTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTA 420
|||||
QY 4795 GACCTTTTCAATTTGCCAGGTAAACCACTGACGACTACCGAGAAAAATGTTTCAAGCTC 4854
|||||
Db 421 GACCTTTTCAATTTGCCAGGTAAACCACTGACGACTACCGAGAAAAATGTTTCAAGCTC 480
|||||
QY 4855 CTCTCTCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCA 4914
|||||
Db 481 CTCTCTCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCG 540
|||||
QY 4915 GATATTGAGGACACCTGAGGAGGCTTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAG 4974
|||||
Db 541 GATGCTGAGGGCTACGTTGAGGAGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 600
|||||
QY 4975 TATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 5034
|||||
Db 601 TATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
|||||
QY 5035 GAAAGAGGAGGAGCTGAGTGGAGGGACGAGGAGGATGAAGAAGGTTATAACGATGAGAG 5094
|||||
Db 661 GAAAGAGGAGGAGCTGAGTGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
|||||
QY 5095 GTAGATGGCGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAAA 5154
|||||
Db 721 GTAGATGAGGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAA 780
|||||
QY 5155 TGAGAACCTGAAGATGAGGAGGAGGAGGATGATGACTAGTGAATAACCTATTGAAAAAT 5214
|||||
Db 781 CGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
|||||
QY 5215 TCCTATTGATTCGACTGTTTTTACCCTATCCCT-----CCCCCTCCAACTCTGCC 5268
|||||
Db 841 TCCTATTGATTCGACTGTTTTTACCCTATCCCTCTCCCCCTCTAATCCTGCC 900
|||||
QY 5269 CCCTGAA 5276
|||||
Db 901 CCCTGAA 908
|||||
RESULT 13
US-10-273-334-30
; Sequence 30, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(455)
; OTHER INFORMATION:
US-10-273-334-30

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Best Local Similarity 90.2%; Pred. No. 4.1e-69;
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RESULT 15
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; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shriharis S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
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; NUMBER OF SEQ ID NOS: 51
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; TYPE: DNA
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; NAME/KEY: CDS
; LOCATION: (64)..(810)
; OTHER INFORMATION:
US-10-273-334-11

Query Match 12.3%; Score 711.8; DB 6; Length 905;
Best Local Similarity 89.9%; Pred. No. 1.8e-67;
Matches 815; Conservative 0; Mismatches 72; Indels 20; Gaps 4;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	866.6	97.5	895	22	US-09-591-500-15	Sequence 15, Appli
4	865	97.3	895	22	US-09-591-500-21	Sequence 21, Appli
5	839.4	94.4	895	22	US-09-591-500-23	Sequence 23, Appli
6	831.4	93.5	907	22	US-09-591-500-6	Sequence 6, Appli
7	764.2	86.0	1197	30	US-09-760-469-94	Sequence 94, Appli
8	764.2	86.0	1197	42	US-10-216-583-94	Sequence 8887, Ap
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27 762.2 85.7 3955 36 US-09-976-594-207 Sequence 207, Ap
28 762.2 85.7 3955 68 US-60-240-409-207 Sequence 207, Ap
29 761 85.6 907 22 US-09-591-500-25 Sequence 25, Appl
30 761 85.6 1052 1 PCT-US02-25766-3866 Sequence 3866, Ap
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36 757.8 85.2 907 22 US-09-591-500-28 Sequence 2, Appl
37 756.2 85.1 916 14 US-09-038-847A-2 Sequence 25, Appl
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42 742 83.5 1155 1 PCT-US01-09631-12193 Sequence 13384, A
43 735.6 82.7 6753 61 US-60-172-373-13384 Sequence 30, Appl
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ALIGNMENTS

RESULT 1
US-09-591-500-3
; Sequence 3, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
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; ORGANISM: Homo sapiens
US-09-591-500-3

Query Match 100.0%; Score 889; DB 22; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.4e-158;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 TCAGCACAATAGAGGCACCTGAACACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
DB 361 TCAGCACAATAGAGGCACCTGAACACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
QY 421 GCGAGGTAAACCAACCTGAACAGCTACGAGAGAAAACGTGTTCAAGCTTCTCTGCAACTCA 480
DB 421 GCGAGGTAAACCAACCTGAACAGCTACGAGAGAAAACGTGTTCAAGCTTCTCTGCAACTCA 480
QY 481 CATATCTCGACAGCTGTACTGGGACCAAGAGAGCCCTTACTCAGATATTGAGGACC 540
DB 481 CATATCTCGACAGCTGTACTGGGACCAAGAGAGCCCTTACTCAGATATTGAGGACC 540
QY 541 ACCTGGAGGGCCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGTATGATGAAGATG 600
DB 541 ACCTGGAGGGCCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGTATGATGAAGATG 600
QY 601 CTCAGGTAGTGGAAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 CTCAGGTAGTGGAAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 TGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATACGATGAGAGGTAGATGGCGAGG 720
DB 661 TGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATACGATGAGAGGTAGATGGCGAGG 720
QY 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAGCGGAAATGAGAACCTCAAG 780
DB 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAGCGGAAATGAGAACCTCAAG 780
QY 781 ATGAGGAGAGAGATGATGACTAGTAGATAAAGTATTTTGAAGAAATTCCTATTGTGATT 840
DB 781 ATGAGGAGAGAGATGATGACTAGTAGATAAAGTATTTTGAAGAAATTCCTATTGTGATT 840
QY 841 TGACTGTTTTTACCATATCCCTCCCTCCCAATCCTCCCTCCCTGAA 889
DB 841 TGACTGTTTTTACCATATCCCTCCCTCCCAATCCTCCCTGAA 889

RESULT 2
US-09-591-500-1
; Sequence 1, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5785
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (4453)..(5154)
; OTHER INFORMATION:
US-09-591-500-1

```
Query Match      100.0%; Score 889; DB 22; Length 5785;
Best Local Similarity 100.0%; Pred. No. 1.8e-158;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
Db 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 4447

QY 61 GAGAGATGGAGATGGGACAGCGGATTTCATTTCAGAGCTGCGGAACAGAGCGCCCTCTCATG 120
Db 4448 GAGAGATGGAGATGGGACAGCGGATTTCATTTCAGAGCTGCGGAACAGAGCGCCCTCTCATG 4507

QY 121 TGAAGAACTTGGCCTGACACACAGTGGTTCGAATGAAGCAAACTCGAAGCCCTCACAG 180
Db 4508 TGAAGAACTTGGCCTGACACACAGTGGTTCGAATGAAGCAAACTCGAAGCCCTCACAG 4567

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240
Db 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 4627

QY 241 ACTTACCAAACTTAAAGTTGAGAAGCTTGAACCTTAAGAGTCTCAGGGGCTGGAAGTAT 300
Db 4628 ACTTACCAAACTTAAAGTTGAGAAGCTTGAACCTTAAGAGTCTCAGGGGCTGGAAGTAT 4687

QY 301 TGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAGAGCC 360
Db 4688 TGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAGAGCC 4747

QY 361 TCAGCAACAATAGAGCCACTGAACAGTTTGAACACCTCAAGAGCTTAGACCTTTTCAATT 420
Db 4748 TCAGCAACAATAGAGCCACTGAACAGTTTGAACACCTCAAGAGCTTAGACCTTTTCAATT 4807

QY 421 GCGAGGTAAACCAACTGAACGACTACGAGGAGAAAGCTTCAAGCTTCTCTCCACTCA 480
Db 4808 GCGAGGTAAACCAACTGAACGACTACGAGGAGAAAGCTTCAAGCTTCTCTCCACTCA 4867

QY 481 CATATCTCGACAGCTGTACTTGGACACAAAGGAGGCCCTTACTCAGATATTCAGAGCC 540
Db 4868 CATATCTCGACAGCTGTACTTGGACACAAAGGAGGCCCTTACTCAGATATTCAGAGCC 4927

QY 541 ACGTGGAGGGCTGGATGACGAGGAGAGGGTGAGCATGAGGAGGTATGATGAAGATG 600
Db 4928 ACGTGGAGGGCTGGATGACGAGGAGAGGGTGAGCATGAGGAGGTATGATGAAGATG 4987

QY 601 CTCAGGTAGTGGAGATGAGGAGGGCGGAGGAGGAGGAGGAGGTGAAGAGGAGGAGC 660
Db 4988 CTCAGGTAGTGGAGATGAGGAGGGCGGAGGAGGAGGAGGAGGTGAAGAGGAGGAGC 5047

QY 661 TGAGTGGAGGGAGGAGGAGGTGAAGAGGTATTAACGATGGAGAGGTAGATGGCGAGG 720
Db 5048 TGAGTGGAGGGAGGAGGAGGTGAAGAGGTATTAACGATGGAGAGGTAGATGGCGAGG 5107

QY 721 AAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTTCAGAGCGGAAATGAGACCTCAAG 780
Db 5108 AAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTTCAGAGCGGAAATGAGACCTCAAG 5167

QY 781 ATGAGGAGAGAGATGATGACTAAGTAACTATTTTGAAGAAATTCCTATTGTGATT 840
Db 5168 ATGAGGAGAGAGATGATGACTAAGTAACTATTTTGAAGAAATTCCTATTGTGATT 5227

QY 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCAATCTCGCCCTCGAA 889
Db 5228 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCAATCTCGCCCTCGAA 5276
```

RESULT 3
US-09-591-500-15
; Sequence 15, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkoi, Shrihari S.

```
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY  
; FILE REFERENCE: 031787.0076  
; CURRENT APPLICATION NUMBER: US/09/591,500  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: PCT/US98/26433  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: US 60/069,677  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 895  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (66)..(767)  
; OTHER INFORMATION:  
US-09-591-500-15
```

```
Query Match      97.5%; Score 866.6; DB 22; Length 895;  
Best Local Similarity 99.4%; Pred. No. 2.5e-154;  
Matches 868; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60  
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60  
  
QY 61 GAGAGATGGAGATGGCAGACGGATTTCATTTCAGAGCTGCGGAACAGGCGCCCTCTCATG 120  
Db 61 GAGAGATGGAGATGGCAGACGGATTTCATTTCAGAGCTGCGGAACAGGCGCCCTCTCATG 120  
  
QY 121 TGAAGAACTTGGCCTGGACACAGTTCGGTTCGAATGAAGCAAACTCGAAGCCCTCACAG 180  
Db 121 TGAAGAACTTGGCCTGGACACAGTTCGGTTCGAATGAAGCAAACTCGAAGCCCTCACAG 180  
  
QY 181 ATGAATTTCAAGAACTTGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240  
Db 181 ATGAATTTCAAGAACTTGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240  
  
QY 241 ACTTACCAAACTTAAAGTTGAGAAAGCTTGAACCTCAAGAGTCTCAGGGGCTTGAAGTAT 300  
Db 241 ACTTACCAAACTTAAAGTTGAGAAAGCTTGAACCTCAAGAGTCTCAGGGGCTTGAAGTAT 300  
  
QY 301 TGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAGAGCC 360  
Db 301 TGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAGAGCC 360  
  
QY 361 TCAGCAACAATAGAGCCACTGAAACAGTTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420  
Db 361 TCAGCAACAATAGAGCCACTGAAACAGTTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420  
  
QY 421 GCGAGGTAAACCAACTGAAAGCTACGGAAGAAAGCTGTTCAAGCTTCTCTGCAACTCA 480  
Db 421 GCGAGGTAAACCAACTGAAAGCTACGGAAGAAAGCTGTTCAAGCTTCTCTGCAACTCA 480  
  
QY 481 CATATCTCGACAGCTGTACTTGGACACCAAGGAGGCCCTTACTCAGATATTCAGAGCC 540  
Db 481 CATATCTCGACAGCTGTACTTGGACACCAAGGAGGCCCTTACTCAGATATTCAGAGCC 540  
  
QY 541 ACGTGGAGGGCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGTATGATGAAGATG 600  
Db 541 ACGTGGAGGGCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGTATGATGAAGATG 600  
  
QY 601 CTCAGGTAGTGAAGATGAGGAGGGCGGAGGAGGAGGAGGAGGTGAAGAGGAGGAGC 660  
Db 601 CTCAGGTAGTGAAGATGAGGAGGGCGGAGGAGGAGGAGGAGGTGAAGAGGAGGAGC 660  
  
QY 661 TGAGTGGAGGGAGCAGGAGGAGGTGAAGAGGTATTAACGATGGAGAGGTAGATGCGGAGG 720  
Db 661 TGAGTGGAGGGAGCAGGAGGAGGTGAAGAGGTATTAACGATGGAGAGGTAGATGCGGAGG 720  
  
QY 721 AAGATGAAGAGAGAGCTTGGTGAAGAGAAAGGGTTCAGAGCGGAAATGAGAACCTGAAG 780
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Db 721 RAGATGAAGAGAGCTTGGTGAAGAAGAAAGGGTCAAGCGCAAAATGAGAACCTGAAG 780
QY 781 ATGAGGGAGAGATGATGACTAAAGTAGAATAACCTATTGTAAGAAATTCCTATTGTGATT 840
Db 781 ATGAGGGAGAGATGATGACTAAAGTAGAATAACCTATTGTAAGAAATTCCTATTGTGATT 840
QY 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCC 873

RESULT 4
US-09-591-500-21
; Sequence 21, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-09-591-500-21

Query Match 97.3%; Score 865; DB 22; Length 895;
Best Local Similarity 99.3%; Pred. No. 5.le-154;
Matches 867; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCAGAGAGCTCTGCAGACAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGCAGACGAGATTCAATTCAGAGCTGCGGAACAGGGCGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCAGACGAGATTCAATTCAGAGCTGCGGAACAGGGCGCCCTCTGATG 120
QY 121 TGAAGAACTTGCCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCAG 180
Db 121 TGAAGAACTTGTCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCAG 180
QY 181 ATCAATTTGAAGAACTTGAATTTTAAAGTAAATCAACGAGGCTCACTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTTGAATTTTAAAGTAAATCAACGAGGCTCACTCAATCTCAG 240
QY 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTTGAAGTCTCAGGGGGCTTGAAGTAT 300
Db 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTTGAAGTCTCAGGGGGCTTGAAGTAT 300
QY 301 TGGCAGAAAGTGTCCAAACCTCAGGCATCTATATTAAAGTGGCAACAAATTAAGACC 360
Db 301 TGGCAGAAAGTGTCCAAACCTCAGGCATCTATATTAAAGTGGCAACAAATTAAGACC 360
QY 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTAGACCTTTTCAATT 420
Db 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTAGACCTTTTCAATT 420
QY 421 GCGAGGTAAACCACTGAAACGACTACGGAGAAAACGTTGTTCAAGCTTCTCCTGCAACTCA 480
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Db 421 GCGAGGTAAACCACTGAAACGACTACGGAGAAAACGTGTTCAAGCTTCTCCTGCAACTCA 480
QY 481 CATATCTCGACACTCTTACTGGACCCACAGAGAGCCCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACACTCTTACTGGACCCACAGAGAGCCCTTACTCAGATATTGAGGACC 540
QY 541 ACCTGGAGGCGCTTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATG 600
Db 541 ACCTGGAGGCGCTTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATG 600
QY 601 CTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 601 CTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 TGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGGTAGATGGCGAGG 720
Db 661 TGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGGTAGATGGCGAGG 720
QY 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGGAAATGAGAACCTGAAG 780
Db 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGGAAATGAGAACCTGAAG 780
QY 781 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTGTAAGAAATTCCTATTGTGATT 840
Db 781 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTGTAAGAAATTCCTATTGTGATT 840
QY 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCC 873

RESULT 5
US-09-591-500-23
; Sequence 23, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-09-591-500-23

Query Match 94.4%; Score 839.4; DB 22; Length 895;
Best Local Similarity 97.5%; Pred. No. 3.6e-149;
Matches 851; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGACAGAGAGCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCAGAGAGCTCTGCAGAGAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGCAGAGCGGATTCAATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCAGAGCGGATTCAATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120
QY 121 TGAAGAACTTGCCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCAG 180
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Db 121 TGAAGAAGACTGTCTCGACAACAGTCGGTCGAATGAAGCAACACTCGAAGGCTCACAG 180
Qy 181 ATGAATTTGAAGAACTGGAATCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTGGAATCTTAAGTAAATCAACAGTAGGCTCACCTCAATCGCAA 240
Qy 241 ACTTACCAAAAGTTAAAGTTGAGAAGCTTGAACCTAAGCAGTCTCAGGGGCTCGAAGTAT 300
Db 241 ACTTACCAAAAGTTAAAGTTGAGAAGCTTGAACCTAAGCAGTCTCAGGGGCTCGAAGTAT 300
Qy 301 TGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAGAGACC 360
Db 301 TGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAGAGACC 360
Qy 361 TCAGCAATAAGAGCCACTGAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATT 420
Db 361 TCAGCAATAAGAGCCACTGAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATT 420
Qy 421 GCGAGGTAACCAACCTGAAGGACTTACGAGAAACAGTGTTCAGACTTCTCCTGCAACTCA 480
Db 421 GCGAGGTAACCAACCTGAAGGACTTACGAGAAACAGTGTTCAGACTTCTCCTGCAACTCA 480
Qy 481 CATATCTCGACAGCTGTACTTGGGACCAAGAGGCCCCCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACAGCTGTACTTGGGACCAAGAGGCCCCCTTACTCAGATATTGAGGACC 540
Qy 541 ACGTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGATGATGAAGATG 600
Db 541 ACGTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGATGATGAAGATG 600
Qy 601 CTCAGGTAGTGGAAAGTACGAGGCGGAGGAGGAGGAGGAGTGAAGAGGAGGAGC 660
Db 601 CTCAGGTAGTGGAAAGTACGAGGCGGAGGAGGAGGAGGAGTGAAGAGGAGGAGC 660
Qy 661 TGAGTGAGGCGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGGTAGATGCGAGG 720
Db 661 TGAGTGAGGCGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGGTAGATGCGAGG 720
Qy 721 AAGATGAAGAGAGCTGTGGTGAAGAAAGGGGTGAGAGCGGAAATGAGAACCTTGAAG 780
Db 721 AAGATGAAGAGAGCTGTGGTGAAGAAAGGGGTGAGAGCGGAAATGAGAACCTTGAAG 780
Qy 781 ATGAGGAGAGAGTATGATGACTAAGTGAATAACCTATTTTGAATAATTCCTATTGTGATT 840
Db 781 ATGAGGAGAGAGTATGATGACTAAGTGAATAACCTATTTTGAATAATTCCTATTGTGATT 840
Qy 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCC 873

RESULT 6
US-09-591-500-6
; Sequence 6, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkoi, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 907
; TYPE: DNA

i ORGANISM: Homo sapiens
US-09-591-500-6

Query Match 93.5%; Score 831.4; DB 22; Length 907;
Best Local Similarity 97.4%; Pred. No. 1.2e-147;
Matches 883; Conservative 0; Mismatches 6; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTGGCTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGAGGTTTATTGATTGGCTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
Qy 61 GAGAGATGAGATGGCAGCAGGATTCATTTCAGAGCTCGGAACAGGCGCCCTCTGATG 120
Db 61 GAGAGACGAGATGGCAGCAGGATTCATCTAGAGCTCGGAACAGGCGCCCTCTGATG 120
Qy 121 TGAAGAAGCTTCCCTGGACACAGTCGCTCGAATGAAGCAAACTCGAAGCCCTCACAG 180
Db 121 TGAAGAAGCTTCCCTGGACACAGTCGCTCGAATGAAGCAAACTCGAAGCCCTCACAG 180
Qy 181 ATCAATTTGAAGAACTTGAATTTCTTAAGTAAATCAACGAGGCGCTCACCCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAAGCTTGAATTTCTTAAGTAAATCAACGAGGCGCTCACCCTCAATCTCAG 240
Qy 241 ACTTACCAAAAGTTA--AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
Db 241 ACTTACCAAAAGTTAACAAGTTGAGAAAGCTTGAAGAGCTTAACAGAGTCTCAGGG 300
Qy 289 GCGTGGAAAGTATTGGCAGAAAAGTGTCCAACCTCACGCATCTATATTTAAGTGGCAACA 348
Db 301 GCGTGGAAAGTATTGGCAGAAAAGTGTCCAACCTCACGCATCTATATTTAAGTGGCAACA 360
Qy 349 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 361 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 420
Qy 409 ACCTTTTCAATTCGAGGTTAACCAACCTCAAGGACTAGCGAGAAACCTGTTCAGAGTTC 468
Db 421 ACCTTTTCAATTCGAGGTTAACCAACCTCAAGGACTAGCGAGAAACCTGTTCAGAGTTC 480
Qy 469 TCCTGCAACTACATATCTCGACAGCTGTACTGGGACCACAAGGAGGCCCTTACTCAG 528
Db 481 TCCTGCAACTACATATCTCGACAGCTGTACTGGGACCACAAGGAGGCCCTTACTCAG 540
Qy 529 ATATTGAGGACCACTGGAGGCGCTGGATGACGAGGAGGAGGCTCAGCATGAGGAGGAGT 588
Db 541 ATATTGAGGCGCCACCTGGAGGCGCTGGATGACGAGGAGGAGGCTCAGCATGAGGAGGAGT 600
Qy 589 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGT 648
Db 601 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGT 660
Qy 649 AAGAGGAGCAGTGTAGTGGAGGACGAGGAGGATGAAGAAGGTTTAAACGATGGAGAGG 708
Db 661 AAGAGGAGCAGTGTAGTGGAGGACGAGGAGGATGAAGAAGGTTTAAACGATGGAGAGG 720
Qy 709 TAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAGAAAGGGGTGAGAAAGGCGAAAT 768
Db 721 TAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAGAAAGGGGTGAGAAAGGCGAAAT 780
Qy 769 GAGAACCTGAAGATGAGGAGGAAGATGACTAAGTGAATAACCTATTTTGAATAAT 828
Db 781 GAGAACCTGAAGATGAGGAGGAAGATGACTAAGTGAATAACCTATTTTGAATAAT 840
Qy 829 CCTATTGTGATTGACTGTGTTTTACCATATCCCT-----CCCCCTCCAACTCTGCC 882
Db 841 CCTATTGTGATTGACTGTGTTTTACCATATCCCTCTCCCCCCCCCTCTAACTCTGCC 900
Qy 883 CCTCGAA 889
Db 901 CCTCGAA 907

RESULT 7

```
US-09-760-469-94
; Sequence 94, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; PRIOR FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-760-469-94

Query Match      86.0%; Score 764.2; DB 30; Length 1197;
Best Local Similarity 92.7%; Pred. No. 6.7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGCGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
DB 94 GGGTTCGAGGTTTATTGATTGAATTCGGCTGCGCAGCAGAGCCTCTGCAGACAGAGAGCGC 153
QY 61 GAGAGATGAGATGGCGACGAGGATTTCATTTCAGAGCTCGGGAACAGGCGCCCTCTGATG 120
DB 154 GAGAGATGAGATGGCGACGAGGATTTCATTTCAGAGCTCGGGAACAGGAGCGCCCTCTGATG 213
QY 121 TGAAGAACTTCCCTCGGACGAGCTCGGTGCGAATGAAGGCAAACTCGAAGCCCTCAG 180
DB 214 TGAAGAACTTCCCTCGGACGAGCTCGGTGCGAATGAAGGCAAACTCGAAGCCCTCAG 273
QY 181 ATGAATTTCAAGAACTTGAATTTCTTAAGTAAATCAACGAGGCGCTCACTCAATCTCAG 240
DB 274 ATGAATTTGAAGAACTGGAATTTCTTAAGTAACTCAAGTAGGCGCTCACTCAATCTCAG 333
QY 241 ACTTACCAAGTTA---AAGTTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGG 288
DB 334 ACTTACCAAGTTAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAG 393
QY 289 GCCTGGAAGTATGGCAGAAAGTGTCCAAACCTCAGCACTATATTTAAGTGCAACA 348
DB 394 GCCTGGAAGTATGGCAGAAAGTGTCCAAACCTCAGCACTATATTTAAGTGCAACA 453
QY 349 AAATTAAGACCTCAGCACAATAGAGCCACTCAAAACAGTTAGAAAACCTCAAGAGCTTAG 408
DB 454 AAATTAAGACCTCAGCACAATAGAGCCACTCAAAACAGTTAGAAAACCTCAAGAGCTTAG 513
QY 409 ACCTTTTCAATTCGAGAGTTAACCAACCTGAACGACTACGGAGAAAACGTTTCAAGCTTC 468
DB 514 ACCTTTTCAATTCGAGAGTTAACCAACCTGAACGACTACGGAGAAAACGTTTCAAGCTTC 573
QY 469 TCCTGCAACTCACAATCTCGACAGCTGTTACTGGGACACAGGAGGCCCTTACTCAG 528
DB 574 TCCTGCAACTCACAATCTCGACAGCTGTTACTGGGACACAGGAGGCCCTTACTCAG 633
QY 529 ATATTTCAGGACACAGCTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGGATGAGGAGG 588
DB 634 ATGCTCAGGCTACGTTGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 693
QY 589 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGTGTG 648
DB 694 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGTGTG 753
QY 649 AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGATCAAGAACTTATACGATGAGAGG 708
DB 754 AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGATCAAGAACTTATACGATGAGAGG 813
QY 709 TAGATGGCGAGGAAGATGAAGAGAGCTTTGGTGAAGAAAGAGGGGTCAAGAGCGGAAAT 768
DB 814 TAGATGACGAGGAAGATGAAGAGAGCTTTGGTGAAGAAAGAGGGGTCAAGAGCGGAAAC 873
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```
QY 769 GAGAACCTGAAGATGAGGAGAGAGATGACTAAGTAACTAAGTAACCTATTTTGAATAATT 828
DB 874 GAGAACCTGAAGATGAGGAGAGAGATGACTAAGTAACTAAGTAACCTATTTTGAATAATT 933
QY 829 CCTATTGTGATTGACTGTGTTTTACCCATATCCCT-----CCCCCTCCCAATCTCGCC 882
DB 934 CCTATTGTGATTGACTGTGTTTTACCCATATCCCTCTCCCTCCCTCCCAATCTCGCC 993
QY 883 CCCTGAA 889
DB 994 CCCTGAA 1000

RESULT 8
US-10-216-583-94
; Sequence 94, Application US/10216583
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254CIN
; CURRENT APPLICATION NUMBER: US/10/216,583
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,469
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-583-94

Query Match      86.0%; Score 764.2; DB 42; Length 1197;
Best Local Similarity 92.7%; Pred. No. 6.7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGCGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
DB 94 GGGTTCGAGGTTTATTGATTGAATTCGGCTGCGCAGCAGAGCCTCTGCAGACAGAGAGCGC 153
QY 61 GAGAGATGAGATGGCGACGAGGATTTCATTTCAGAGCTCGGGAACAGGCGCCCTCTGATG 120
DB 154 GAGAGATGAGATGGCGACGAGGATTTCATTTCAGAGCTCGGGAACAGGAGCGCCCTCTGATG 213
QY 121 TGAAGAACTTCCCTCGGACGAGCTCGGTGCGAATGAAGGCAAACTCGAAGCCCTCAG 180
DB 214 TGAAGAACTTCCCTCGGACGAGCTCGGTGCGAATGAAGGCAAACTCGAAGCCCTCAG 273
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
DB 274 ATGAATTTGAAGAACTGGAATTTCTTAAGTAACTCAAGTAGGCGCTCACCTCAATCTCAG 333
QY 241 ACTTACCAAGTTA---AAGTTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGG 288
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Db	334	ACTTACC	AAAGTTAA	CAAACTTA	GAAGGCTT	GAACGTAA	GCAGATA	CACAGAGTCT	TCAGGG	393			
QY	289	GCCTG	GAAGTATT	GGCAG	AAAAAGT	GTCCAA	ACCTC	ACGCA	TCATATTTA	AGTG	CA	348	
Db	394	GCCTG	GAAGTATT	GGCAG	AAAAAGT	GCCGA	ACCTC	ACGCA	CTTAATTTA	AGTG	CA	453	
QY	349	AAATTA	AGACCTC	AGCACA	CAATTA	GAGCC	ACTGA	AAACCTTAG	AAAACTT	CA	AGAGCTT	AG	408
Db	454	AAATTA	AGACCTC	AGCACA	CAATTA	GAGCC	ACTGA	AAACCTTAG	AAAACTT	CA	AGAGCTT	AG	513
QY	409	ACCTTTT	CAATTC	GGAGGT	TAACCA	ACCTGA	ACGACTAC	GGAGAAAA	ACGTGTTT	CA	AGCTTC	TC	468
Db	514	ACCTTTT	CAATTC	GGAGGT	TAACCA	ACCTGA	ACGACTAC	GGAGAAAA	ACGTGTTT	CA	AGCTTC	TC	573
QY	469	TCC	TGCAACT	TCACATAT	CTCG	ACAGCTGT	TACTGG	GACCA	CACAG	AGGCCCTT	ACT	AC	528
Db	574	TCCG	CAACTC	ACATATCT	CGACGG	CTATG	ACCCGG	GACCA	CAGGAG	GGCCCTG	ACT	CGG	633
QY	529	ATATT	GAGGAC	CACTG	TGGAGG	CGCTGG	ATCACC	AGCAG	GAGG	GGTGAC	ATGAGG	AGGAGT	588
Db	634	ATGCT	GAGG	CGCTG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	693
QY	589	ATGAT	GAAGAT	GTCTC	AGGTAGT	GGAA	AGATGAG	AGGCGG	AGGAGG	AGGAGG	AGGAGG	AGGAGG	648
Db	694	ATGAT	GAAGAT	GTCTC	AGGTAGT	GGAA	AGATGAG	AGGCGG	AGGAGG	AGGAGG	AGGAGG	AGGAGG	753
QY	649	AAGAG	GAGAC	CTGATG	TGGAGG	GCAG	AGGAGG	ATGA	AGAGG	TTATAC	GCATG	GCAGAGG	708
Db	754	AAGAG	GAGAC	CTGATG	TGGAGG	GCAG	AGGAGG	ATGA	AGAGG	TTATAC	GCATG	GCAGAGG	813
QY	709	TAGAT	GCGAG	GAA	GATGA	AGAGAG	CTTGGT	GCAAG	AAAGGG	GTGAC	AGACG	CGAAT	768
Db	814	TAGAT	GCGAG	GAA	GATGA	AGAGAG	CTTGGT	GCAAG	AAAGGG	GTGAC	AGACG	CGAAT	873
QY	769	GAGA	CACTGA	AGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	828
Db	874	GAGA	CACTGA	AGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	ATGATG	933
QY	829	CC	TATTG	TGATTT	GACTG	TTTTT	TAC	CCATAT	CCCC	T-----	CCCC	CTCC	882
Db	934	CC	TATTG	TGATTT	GACTG	TTTTT	TAC	CCATAT	CCCC	T-----	CCCC	CTCC	993
QY	883	CCCT	GTAA	889									
Db	994	CCCT	GTAA	1000									

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RESULT 9
US-09-644-871-8887
; Sequence 8887, Application US/09644871
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1167-001
; CURRENT APPLICATION NUMBER: US/09/644, 871
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151,059
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 9739
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8887
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-644-871-8887

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Query Match 86.0%; Score 764.2; DB 25; Length 1595;

[illegible]

RESULT 10
US-09-649-164-9117
; Sequence 9117, Application US/09649164
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.

```
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: THEREFOR
; FILE REFERENCE: 1600.1165.001
; CURRENT APPLICATION NUMBER: US/09/649,164
; PRIOR FILING DATE: 2000-08-25
; APPLICATION NUMBER: 60/150,606
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 9995
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9117
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-649-164-9117
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Query Match      86.0%; Score 764.2; DB 25; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;
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```
QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
Db 257 CGGTTCCGGGTTTATTGATTGAATTCGGCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 316
QY 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGGACAGAGCGCCCTCTGATG 120
Db 317 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGGACAGAGCGCCCTCTGATG 376
QY 121 TGAAGAAGCTTCGCCCTGGCAACACAGTCGGTGAATGAAGGCAAACTCGAAGCCTCACAG 180
Db 377 TGAAGAAGCTTCGCCCTGGCAACACAGTCGGTGAATGAAGGCAAACTCGAAGCCTCACAG 436
QY 181 ATGAATTTGAAGAAGCTTGAATTTTAAAGTAAATCAACGAGAGGCTCACTCAATCTCAG 240
Db 437 ATGAATTTGAAGAAGCTTGAATTTTAAAGTAAATCAACGAGAGGCTCACTCAATCTCAG 496
QY 241 ACTTACCAAGTTA---AGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
Db 497 ACTTACCAAGTTAACCAAACTTAAAGAGAGCTTGAACCTAAGCGATAACAGAGTCTCAGGGG 556
QY 289 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTTCAGCATCTATATTTAAGTGGCAACA 348
Db 557 GCCTGGAAGTATTGGCAGAAAAGTGTCCGAACTCAGCATCTAANTTTAAGTGGCAACA 616
QY 349 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGATTAGAAAACCTCAAGAGCTTAG 408
Db 617 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGATTAGAAAACCTCAAGAGCTTAG 676
QY 409 ACCTTTTCAATTGCGAGGTAACCAACCTGACGACTACGAGAGAAACCTGTTCAGGCTTC 468
Db 677 ACCTTTTCAATTGCGAGGTAACCAACCTGACGACTACGAGAGAAACCTGTTCAGGCTTC 736
QY 469 TCCTGCAACTCACAATCTCGACAGCTGTACTGGGACCAACAGAGGCGCCCTTACTCAG 528
Db 737 TCCTGCAACTCACAATCTCGACAGCTGTACTGGGACCAACAGAGGCGCCCTGACTCGG 796
QY 529 ATATTGAGACCAAGTGGAGGCGCTGGATGACGAGGAGGAGGGGTGACCATGAGGAGGAGT 588
Db 797 ATGCTGAGGCGCTACCTGGAGGCGCTGGATGATGAGGAGGAGGAGTGAAGTGAAGGAGT 856
QY 589 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 648
Db 857 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 916
QY 649 AAGAGGAGGACCTGATGGAGGCGACGAGGAGGATCAAGAAGTTTAAACGATGGAGAGG 708
Db 917 AAGAGGAGGACCTGATGGAGGCGACGAGGAGGATCAAGAAGTTTAAACGATGGAGAGG 976
QY 709 TAGATGGCAGGAGAGTGAAGAAGAGCTTGGTGAAGAGAGAAAGGGGTGAGAGGCGAAAT 768
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Db 977 TAGATGACGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTGAGAGCGGAAAC 1036
QY 769 GAGAACTGAAGATGAGGAGAGATGATGACTAAGTAACTAAGTAACCTATTTTGAATAATT 828
Db 1037 GAGAACTGAAGATGAGGAGAGATGATGACTAAGTAACTAAGTAACCTATTTTGAATAATT 1096
QY 829 CCTATTGTGATTTGACTGTGTTTACCATATCCCTC-----CCCCCTCCAAATCCTGCC 882
Db 1097 CCTATTGTGATTTGACTGTGTTTACCATATCCCTC-----CCCCCTCCAAATCCTGCC 1156
QY 883 CCTGTAA 889
Db 1157 CCTGTAA 1163

RESULT 11
US-09-652-913-10130
; Sequence 10130, Application US/09652913
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean R.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: THEREFOR
; FILE REFERENCE: 1600.1174-001
; CURRENT APPLICATION NUMBER: US/09/652,913
; PRIOR FILING DATE: 2000-08-31
; APPLICATION NUMBER: 60/152,107
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 10833
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10130
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-913-10130
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Query Match      86.0%; Score 764.2; DB 25; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;
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```
QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
Db 257 GGGTTCGGGTTTATTGATTGAATTCGGCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 316
QY 61 GAGAGATGGAGATGGGAGAGCGGATTTCATTCAGAGCTCGGGAACAGGCGCCCTCTGATG 120
Db 317 GAGAGATGGAGATGGGAGAGCGGATTTCATTCAGAGCTCGGGAACAGGCGCCCTCTGATG 376
QY 121 TGAAGAAGCTTCGCCCTGGCAACACAGTCGGTGAATGAAGGCAAACTCGAAGCCTCACAG 180
Db 377 TGAAGAAGCTTCGCCCTGGCAACACAGTCGGTGAATGAAGGCAAACTCGAAGCCTCACAG 436
QY 181 ATGAATTTGAAGAAGCTTGAATTTTAAAGTAAATCAACGAGGAGGCTCACTCAATCTCAG 240
Db 437 ATGAATTTGAAGAAGCTTGAATTTTAAAGTAAATCAACGAGGAGGCTCACTCAATCTCAG 496
QY 241 ACTTACCAAGTTA---AGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
Db 497 ACTTACCAAGTTAACCAAACTTAAAGAGAGCTTGAACCTAAGCGATAACAGAGTCTCAGGGG 556
QY 289 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTTCAGCATCTATATTTAAGTGGCAACA 348
Db 557 GCCTGGAAGTATTGGCAGAAAAGTGTCCGAACTCAGCATCTAANTTTAAGTGGCAACA 616
QY 349 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGATTAGAAAACCTCAAGAGCTTAG 408
Db 617 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGATTAGAAAACCTCAAGAGCTTAG 676
QY 409 ACCTTTTCAATTGCGAGGTAACCAACCTGACGACTACGAGAGAAAGGGGTGAGAGGCGAAAT 468
```


Db 677 ACCITTTCAATTCGAGTACCAACCTGACAGCTACCCGAGAAATGTGTTCAAGCTCC 736
Qy 469 TCCTGCAACTCACATATCTGCAGCTGTACTGGACCAACAAGAGGCCCTTACTCAG 528
Db 737 TCCGCAACTCACATATCTGCAGCTGTACTGGACCAACAAGAGGCCCTTACTCAG 796
Qy 529 ATATTGAGGACCACTGAGGCGCTGGATGACGAGGAGGAGGCTGACATGAGGAGGAGT 588
Db 797 ATGCTGAGGCTACGTGGAGGCGCTGGATGAGGAGGAGGAGTGAAGATGAGGAGGAGT 856
Qy 589 ATGATGAGGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGT 648
Db 857 ATGATGAGGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGT 916
Qy 649 AAGAGGAGGAGTGTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
Db 917 AAGAGGAGGAGTGTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 976
Qy 709 TAGATGCGGAGGAGATGAAGAGAGCTTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGT 768
Db 977 TAGATGCGGAGGAGATGAAGAGAGCTTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGT 1036
Qy 769 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 828
Db 1037 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1096
Qy 829 CCTATTGTGATTGACTGTGTTTACCATAATCCCT-----CCCCCTCCCAATCCCTGCC 882
Db 1097 CCTATTGTGATTGACTGTGTTTACCATAATCCCTCTCCCTCCCTCCCAATCCCTGCC 1156
Qy 883 CCTGAA 889
Db 1157 CCTGAA 1163

RESULT 12
US-09-699-998-8868
; Sequence 8868, Application us/09699998
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2008-001
; CURRENT APPLICATION NUMBER: US/09/699,998
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,362
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 10905
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8868
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-699-998-8868

Query Match 86.0%; Score 764.2; DB 27; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;
Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
Db 257 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 316
Qy 61 GAGAGATGAGATGGGCGAGAGGATTCATTGAGAGCTGCGGAACAGAGGCCCTCTGATG 120
Db 317 GAGAGATGAGATGGGCGAGAGGATTCATTGAGAGCTGCGGAACAGAGAGCCCTCTGATG 376

Qy 121 TGAAGAACTTGCCTGGACACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 377 TGAAGAACTTGCCTGGACAAACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCCTCACAG 436
Qy 181 ATGAATTTGAAGAACTTGAATTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Db 437 ATGAATTTGAAGAACTTGAATTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 496
Qy 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGG 288
Db 497 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGG 556
Qy 289 GCCTGGAAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348
Db 557 GCCTGGAAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 616
Qy 349 AAATTAAGAACCTTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 617 AAATTAAGAACCTTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 676
Qy 409 ACCTTTTCAATTGCGAGGTAAACCACTGAACGACTTACGAGAAAACAGTGTTCAGAGCTTC 468
Db 677 ACCTTTTCAATTGCGAGGTAAACCACTGAACGACTTACGAGAAAACAGTGTTCAGAGCTTC 736
Qy 469 TCCTGCAACTCACATATCTCGACAGCTGTACTGGACCAACAAGAGGCCCTTACTCAG 528
Db 737 TCCTGCAACTCACATATCTCGACAGCTGTACTGGACCAACAAGAGGCCCTTACTCAG 796
Qy 529 ATATTGAGGACCACTGAGGCGCTGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 588
Db 797 ATGCTGAGGCGCTACGTGGAGGCGCTGGATGAGGAGGAGGAGGAGGAGGAGGAGT 856
Qy 589 ATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 648
Db 857 ATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 916
Qy 649 AAGAGGAGGAGTGTAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
Db 917 AAGAGGAGGAGTGTAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 976
Qy 709 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAAAAGGGTCAAGAGCGAAAT 768
Db 977 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAAAAGGGTCAAGAGCGAAAT 1036
Qy 769 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 828
Db 1037 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1096
Qy 829 CCTATTGTGATTGACTGTGTTTACCATAATCCCT-----CCCCCTCCCAATCCCTGCC 882
Db 1097 CCTATTGTGATTGACTGTGTTTACCATAATCCCTCTCCCTCCCTCCCAATCCCTGCC 1156
Qy 883 CCTGAA 889
Db 1157 CCTGAA 1163

RESULT 13
US-09-699-999-6021
; Sequence 6021, Application US/09699999
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Vasicek, Thomas
; APPLICANT: Wang, Youzhan
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2032-001
; CURRENT APPLICATION NUMBER: US/09/699,999
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,361
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 7488

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6021
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-699-999-6021

Query Match      86.0%; Score 764.2; DB 27; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
DB 257 GGGTTTCGGGGTTTATTGATTGAATTCGCCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 316
QY 61 GAGAGATGGAGATGGCAGACGAGTTTCATTACAGAGCTCGGAACAGGCGCCTCTGATG 120
DB 317 GAGAGATGGAGATGGCAGACGAGTTTCATTACAGAGCTCGGAACAGGCGCCTCTGATG 376
QY 121 TGAAGAAGCTTCCCTGGACACAGTCGGTCAATGAAGCAAACTCGAAGCCTCACAG 180
DB 377 TGAAGAAGCTTTCCTGGACACAGTCGGTCAATGAAGCAAACTCGAAGCCTCACAG 436
QY 181 ATCAATTAAGCAAGCTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACTCAATCTCAG 240
DB 437 ATGAATTTGAAGCAAGCTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACTCAATCTCAG 496
QY 241 ACTTACCAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGG 288
DB 497 ACTTACCAAGTTAAGCAAGCTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACTCAATCTCAG 556
QY 289 GCCTGGAAGTATGGCAGAAAAGTGTCCAAACCTACCGCATCTATATTAAAGTGGCAACA 348
DB 557 GCCTGGAAGTATGGCAGAAAAGTGTCCAAACCTACCGCATCTATATTAAAGTGGCAACA 616
QY 349 AAATTAAGACCTCAGCACATAGAGCCACTGAAACACTAGAAACCTCAAGAGCTTAG 408
DB 617 AAATTAAGACCTCAGCACATAGAGCCACTGAAACACTAGAAACCTCAAGAGCTTAG 676
QY 409 ACCTTTCAATTCGAGGTAAACCACTGAACGACTACGAGAGAAAACCTGTTCAAGCTTC 468
DB 677 ACCTTTCAATTCGAGGTAAACCACTGAACGACTACGAGAGAAAATGTGTTCAAGCTTC 736
QY 469 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGAGGCGCCCTTACTCAG 528
DB 737 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGAGGCGCCCTTACTCAG 796
QY 529 ATATTGAGGACCACTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGT 588
DB 797 ATCTGAGGCGTACGTGGAGGCGCTGGATGATGAGGAGGAGGATGAGATGAGGAGGT 856
QY 589 ATGATGAAGATGCTCAGGTAGTGGAGAGTGAAGAGTGAAGGCGGAGGAGGAGGAGGTG 648
DB 857 ATGATGAAGATGCTCAGGTAGTGGAGAGTGAAGAGTGAAGGAGGAGGAGGAGGTG 916
QY 649 AAGAGGAGACGTGAGTGGAGGAGGAGGAGGATGAAGAAGGTATACGATGGAGAGG 708
DB 917 AAGAGGAGACGTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGGTATACGATGGAGAGG 976
QY 709 TAGATGGCGGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAGCGCAAAAT 768
DB 977 TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAGCGCAAAAT 1036
QY 769 GAGAAGCTGAAGATGAGGAGAGATGATGACTAAGTGAATTAACCTATTTTGAAGAAAT 828
DB 1037 GAGAAGCTGAAGATGAGGAGAGATGATGACTAAGTGAATTAACCTATTTTGAAGAAAT 1096
QY 829 CCTATTGCTGACTGTTTTTACCCATATCCCT-----CCGCCCTTCCAAATCCTGCC 882
DB 1097 CCTATTGCTGACTGTTTTTACCCATATCCCTTTCACCCATATCCCTTCCAAATCCTGCC 1156

; GENERAL INFORMATION:
; SEQUENCE 4371, Application US/09710281
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Sbdal, Hilde
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2036-001
; CURRENT APPLICATION NUMBER: US/09710, 281
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164, 254
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 5803
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4371
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-710-281-4371

Query Match      86.0%; Score 764.2; DB 28; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
DB 257 GGGTTTCGGGGTTTATTGATTGAATTCGCCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 316
QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCTCTGATG 120
DB 317 GAGAGATGGAGATGGGAGAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCTCTGATG 376
QY 121 TGAAGAAGCTTCCCTGGACACAGTCGGTCAATGAAGCAAACTCGAAGCCTCACAG 180
DB 377 TGAAGAAGCTTTCCTGGACACAGTCGGTCAATGAAGCAAACTCGAAGCCTCACAG 436
QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACTCAATCTCAG 240
DB 437 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACTCAATCTCAG 496
QY 241 ACTTACCAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGG 288
DB 497 ACTTACCAAGTTAAGCAAGCTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACTCAATCTCAG 556
QY 289 GCCTGGAAGTATGGCAGAAAAGTGTCCAAACCTACCGCATCTATATTAAAGTGGCAACA 348
DB 557 GCCTGGAAGTATGGCAGAAAAGTGTCCAAACCTACCGCATCTATATTAAAGTGGCAACA 616
QY 349 AAATTAAGACCTCAGCACATAGAGCCACTGAAACACTAGAAACCTCAAGAGCTTAG 408
DB 617 AAATTAAGACCTCAGCACATAGAGCCACTGAAACACTAGAAACCTCAAGAGCTTAG 676
QY 409 ACCTTTCAATTCGAGGTAAACCACTGAACGACTACGAGAGAAAACCTGTTCAAGCTTC 468
DB 677 ACCTTTCAATTCGAGGTAAACCACTGAACGACTACGAGAGAAAATGTGTTCAAGCTTC 736
QY 469 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGAGGCGCCCTTACTCAG 528
DB 737 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGAGGCGCCCTTACTCAG 796
QY 529 ATATTGAGGACCACTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGT 588
DB 797 ATCTGAGGCGTACGTGGAGGCGCTGGATGATGAGGAGGAGGATGAGATGAGGAGGT 856
QY 589 ATGATGAAGATGCTCAGGTAGTGGAGAGTGAAGAGTGAAGGCGGAGGAGGAGGAGGTG 648
DB 857 ATGATGAAGATGCTCAGGTAGTGGAGAGTGAAGAGTGAAGGAGGAGGAGGAGGTG 916
QY 649 AAGAGGAGACGTGAGTGGAGGAGGAGGAGGATGAAGAAGGTATACGATGGAGAGG 708
DB 917 AAGAGGAGACGTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGGTATACGATGGAGAGG 976
QY 709 TAGATGGCGGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAGCGCAAAAT 768
DB 977 TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAGCGCAAAAT 1036
QY 769 GAGAAGCTGAAGATGAGGAGAGATGATGACTAAGTGAATTAACCTATTTTGAAGAAAT 828
DB 1037 GAGAAGCTGAAGATGAGGAGAGATGATGACTAAGTGAATTAACCTATTTTGAAGAAAT 1096
QY 829 CCTATTGCTGACTGTTTTTACCCATATCCCT-----CCGCCCTTCCAAATCCTGCC 882
DB 1097 CCTATTGCTGACTGTTTTTACCCATATCCCTTTCACCCATATCCCTTCCAAATCCTGCC 1156
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QY 529 ATATTGAGGACACGCTGGAGGCGCTGGATGACGAGGAGGCGTGAAGATGAGGAGGAGT 588
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Db 797 ATGCTGAGGCTACGTGGAGGCGCTGGATGATGAGGAGGAGATGAGATGAGGAGGAGT 856
QY 589 ATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 648
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Db 857 ATGATGAAGATGCTCAGTGTAGTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGT 916
QY 649 AAGAGGAGGAGTGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
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Db 917 AAGAGGAGGAGTGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 976
QY 709 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGT 768
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Db 977 TAGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGT 1036
QY 769 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 828
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Db 1037 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1096
QY 829 CCTATTGTGATTTGACTGTTTTTACCCTATCCCT-----CCCCCTCAATCCTGCC 882
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Db 1097 CCTATTGTGATTTGACTGTTTTTACCCTATCCCTCTCCCCCCCCCTCCCAATCCTGCC 1156
QY 883 CCCTGAA 889
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Db 1157 CCCTGAA 1163

RESULT 15
US-09-710-286-2968
: Sequence 2968, Application US/09710286
: GENERAL INFORMATION:
: APPLICANT: Gearing, David P.
: APPLICANT: McCarthy, Sean A.
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600,2005-001
: CURRENT APPLICATION NUMBER: US/09710,286
: PRIOR FILING DATE: 2000-11-10
: PRIOR FILING DATE: 1999-11-09
: NUMBER OF SEQ ID NOS: 4115
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2968
: LENGTH: 1595
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)-(1595)
: OTHER INFORMATION: n = A,T,C or G
US-09-710-286-2968

Query Match 86.0%; Score 764.2; DB 28; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCACGAGAGCCCTCTGCAGACAGAGAGCGC 60
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Db 257 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGGCGGAGCCCTCTGCAGAGAGAGAGCGC 316
QY 61 GAGAGATGGAGATGGCGAGACGGATTTCATTCAGAGCTGCGGAACAGAGGCGCCCTCTGATG 120
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 GAGAGATGGAGATGGCGAGACGGATTTCATTCAGAGCTGCGGAACAGAGGCGCCCTCTGATG 376
QY 121 TGAAGAACTTGCCTCGCAACAGTCGGTCGAATGAAGCAAACTCGAAGCCCTCACAG 180
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 TGAAGAACTTGCCTCGCAACAGTCGGTCGAATGAAGCAAACTCGAAGCCCTCACAG 436
QY 181 ATGAATTGAAGAACTGGAATTTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAG 240
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Search completed: December 9, 2002, 00:32:07
Job time : 2152.32 secs

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Db 437 ATGAATTTGAGAACTGGRAATCTTTAAGTACAATCAACGTAGGCGCTCACCTCAATCGCA 496
QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACATA-----AGAGTCTTCAGGGG 288
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Db 497 ACTTACCAAGTTTAAACAAGCTTAAAGAAGCTTGAACATAAGCGGATAACAGAGTCTCAGGG 556
QY 289 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAAACCTCAGCATCTATATTATTTAAGTGGCAACA 348
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 557 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAAACCTCAGCATCTAAATTTAAGTGGCAACA 616
QY 349 AAATTTAAAGACCTCAGCAACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
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Db 617 AAATTTAAAGACCTCAGCAACAATAGAGCCACTGAAAAGTTAGAAAACCTCAAGAGCTTAG 676
QY 409 ACCTTTTCAATTTCGAGGTTAACCAACCTGAACGACTACGAGAAAACGTTGTTCAAGCTTTC 468
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 677 ACCTTTTCAATTTCGAGGTTAACCAACCTGAACGACTACGAGAAAATGTGTTCAAGCTTCC 736
QY 469 TCCTGCAACTCAGATATCTCGACAGCTGTTACTGGGACCACAAAGAGGAGGCGCCCTTACTCAG 528
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Db 737 TCCCGCAACTCAGATATCTCGACGGCTATGACGGGACGACAAAGAGGAGGCGCCCTGACTCGG 796
QY 529 ATATTGAGGACCACTGAGGCGCTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGT 588
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Db 797 ATGCTGAGGCTACGTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 856
QY 589 ATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 648
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Db 857 ATGATGAAGATGCTCAGTGTAGTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGT 916
QY 649 AAGAGGAGGAGTGAAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
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Db 917 AAGAGGAGGAGTGAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 976
QY 709 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGT 768
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Db 977 TAGATGAGGAGGAGATGAAGAGAGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGT 1036
QY 769 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 828
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Db 1037 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1096
QY 829 CCTATTGTGATTTGACTGTTTTTACCCTATCCCT-----CCCCCTCAATCCTGCC 882
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Db 1097 CCTATTGTGATTTGACTGTTTTTACCCTATCCCTCTCCCCCCCCCTCCCAATCCTGCC 1156
QY 883 CCCTGAA 889
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Db 1157 CCCTGAA 1163
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:58:38 ; Search time 55.4388 Seconds
(without alignments)
11105.648 Million cell updates/sec

Title: US-09-591-500-3

Perfect score: 889

Sequence: 1 gggctcgaggtttattgatt.....ctccaatctgcccctgaa 889

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 361435 seqs, 346278564 residues

Total number of hits satisfying chosen parameters: 722870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	889	100.0	889	6	US-10-273-334-3
2	889	100.0	5785	6	US-10-273-334-1
3	866.6	97.5	895	6	US-10-273-334-15
4	865	97.3	895	6	US-10-273-334-21
5	839.4	94.4	895	6	US-10-273-334-23
6	831.4	93.5	907	6	US-10-273-334-6
7	762.6	85.8	907	6	US-10-273-334-13
8	761	85.6	907	6	US-10-273-334-25
9	760.2	85.5	906	6	US-10-273-334-33
10	757.8	85.2	907	6	US-10-273-334-28
11	753	84.7	907	6	US-10-273-334-9
12	751.6	84.5	908	6	US-10-273-334-32
13	727.4	81.8	907	6	US-10-273-334-30
14	716	80.5	907	6	US-10-273-334-4
15	711.8	80.1	905	6	US-10-273-334-11
16	702	79.0	905	6	US-10-273-334-17
17	681.2	76.6	905	6	US-10-273-334-7
18	679.6	76.4	905	6	US-10-273-334-19
19	679.6	76.4	905	6	US-10-273-334-26
20	318.4	35.8	1937	5	US-09-724-676-18913
21	318.4	35.8	1937	5	US-09-724-676A-18913
22	132.6	14.9	147	5	US-09-513-9990-24429
23	110	12.4	3489	6	US-10-194-046-1
24	103.2	11.6	648	6	US-10-152-319A-2106
c 25	101	11.4	659158	5	US-09-771-208A-20
26	100.2	11.3	318	5	US-09-513-9990-14277

ALIGNMENTS

RESULT 1

US-10-273-334-3

; Sequence 3, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kochevar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shrihari S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 031787.0076

; CURRENT APPLICATION NUMBER: US/10/273,334

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 889

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-273-334-3

Query Match . 100.0%; Score 889; DB 6; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.1e-177;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGGTTTCGAGTTTATTGATTGAATTCGCGCTGCACGAGAGCGCTTCGACAGAGAGCGCC	60
Db	1	GGGTTTCGAGTTTATTGATTGAATTCGCGCTGCACGAGAGCGCTTCGACAGAGAGCGCC	60
Qy	61	GAGAGATGGAGATGGGCGACAGCGGATTCATTTCAGAGCTCGGGAACAGGGCGCCCTCTGATG	120
Db	61	GAGAGATGGAGATGGGCGACAGCGGATTCATTTCAGAGCTCGGGAACAGGGCGCCCTCTGATG	120
Qy	121	TGAAGAAGTTCGCTTCGGACACACATCGGTGCGAATGAAGGCAAACTCGAAGCCCTCACAG	180
Db	121	TGAAGAAGTTCGCTTCGGACACACATCGGTGCGAATGAAGGCAAACTCGAAGCCCTCACAG	180
Qy	181	ATGAATTTCAAGAACTGGGAATTTCTTAAGTAAATCAACGAGCGCTTCACCTCAATCTCAG	240
Db	181	ATGAATTTCAAGAACTGGGAATTTCTTAAGTAAATCAACGAGCGCTTCACCTCAATCTCAG	240
Qy	241	ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGGCGCTTGGGAAGTAT	300
Db	241	ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGGCGCTTGGGAAGTAT	300

QY 301 TGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAAATTTAAAGACC 360
Db 301 TGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAAATTTAAAGACC 360
QY 361 TCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTTAGACCTTTTCAATT 420
Db 361 TCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTTAGACCTTTTCAATT 420
QY 421 GGGAGGTAAACCACTGAACGACTACGGAGAAAACGTTTCAAGCTTCTCTGCAACTCA 480
Db 421 GGGAGGTAAACCACTGAACGACTACGGAGAAAACGTTTCAAGCTTCTCTGCAACTCA 480
QY 481 CATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAGATATTGAGGACC 540
QY 541 ACGTGGAGGGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATG 600
Db 541 ACGTGGAGGGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATG 600
QY 601 CTCAGGTAGTGAAGATGAGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 601 CTCAGGTAGTGAAGATGAGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 TGAGTGGAGGGACGAGGAGGATGAAGAAGTTTATAACGATGGAGAGGTAGATGGCGAGG 720
Db 661 TGAGTGGAGGGACGAGGAGGATGAAGAAGTTTATAACGATGGAGAGGTAGATGGCGAGG 720
QY 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGGAAAATGAGAACCTCAAG 780
Db 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGGAAAATGAGAACCTCAAG 780
QY 781 ATGAGGGAGAAGATGATGACTAAGTAGAATAACCTTATTTGAAAAATTCCTATTGTGATT 840
Db 781 ATGAGGGAGAAGATGATGACTAAGTAGAATAACCTTATTTGAAAAATTCCTATTGTGATT 840
QY 841 TGACTGTTTTTACCACATATCCCTCCCTCCCTCCCAATCTGCCCCCTGAA 889
Db 841 TGACTGTTTTTACCACATATCCCTCCCTCCCTCCCAATCTGCCCCCTGAA 889

RESULT 2
US-10-273-334-1
; Sequence 1, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5785
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4453)..(5154)
; OTHER INFORMATION:
US-10-273-334-1

Query Match 100.0%; Score 889; DB 6; Length 5785;

Best Local Similarity 100.0%; Pred. No. 1.7e-177;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCACGAGAGCCTCTGCACAGAGAGCGCC 60
Db 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCACGAGAGCCTCTGCACAGAGAGCGCC 4447
QY 61 GAGAGATGGAGATGGCAGACGCGATTTCATTCAGAGCTGCGGAACAGGGCGCCCTCTGATG 120
Db 4448 GAGAGATGGAGATGGCAGACGCGATTTCATTCAGAGCTGCGGAACAGGGCGCCCTCTGATG 4507
QY 121 TGAAGAACCTTGCCCTGGGACACAGCTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 4508 TGAAGAACCTTGCCCTGGGACACAGCTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 4567
QY 181 ATCAATTTGGAAGAACTTGGAAATTCCTTAAGTAAATCAACGGAGCCCTCACCTCAATCTCAG 240
Db 4568 ATCAATTTGGAAGAACTTGGAAATTCCTTAAGTAAATCAACGGAGCCCTCACCTCAATCTCAG 4627
QY 241 ACTTACCAAGTTTAAAGTTGAGAAAGCTTGAACTAAGAGTCTCAGGGGCGCTGGAAGTAT 300
Db 4628 ACTTACCAAGTTTAAAGTTGAGAAAGCTTGAACTAAGAGTCTCAGGGGCGCTGGAAGTAT 4687
QY 301 TGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAAATTTAAAGACC 360
Db 4688 TGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAAATTTAAAGACC 4747
QY 361 TCAGCAAAATAGAGCCACTGAAACAGTTGAAACCTCAAGAGCTTTAGACCTTTTCAATT 420
Db 4748 TCAGCAAAATAGAGCCACTGAAACAGTTGAAACCTCAAGAGCTTTAGACCTTTTCAATT 4807
QY 421 GCGAGGTAAACCAACCTGACGACTACGGAGAAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Db 4808 GCGAGGTAAACCAACCTGACGACTACGGAGAAAACGTTTCAAGCTTCTCCTGCAACTCA 4867
QY 481 CATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAGATATTGAGGACC 540
Db 4868 CATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAGATATTGAGGACC 4927
QY 541 ACGTGGAGGGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATG 600
Db 4928 ACGTGGAGGGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATG 4987
QY 601 CTCAGGTAGTGGAAAGATGACGAGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 4988 CTCAGGTAGTGGAAAGATGACGAGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
QY 661 TGACTGGAGGGGACGAGGAGGATCAAGAGGTTTAAACGATGAGAGGTAGATGGCGAGG 720
Db 5048 TGACTGGAGGGGACGAGGAGGATCAAGAGGTTTAAACGATGAGAGGTAGATGGCGAGG 5107
QY 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGGAAAATGAGAACCTGAAG 780
Db 5108 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGGAAAATGAGAACCTGAAG 5167
QY 781 ATGAGGGAGAAGATGATGACTAAGTAGAATAACCTTATTTGAAAAATTCCTATTGTGATT 840
Db 5168 ATGAGGGAGAAGATGATGACTAAGTAGAATAACCTTATTTGAAAAATTCCTATTGTGATT 5227
QY 841 TGACTGTTTTTACCACATATCCCTCCCTCCCTCCCAATCTGCCCCCTGAA 889
Db 5228 TGACTGTTTTTACCACATATCCCTCCCTCCCTCCCAATCTGCCCCCTGAA 5276

RESULT 3
US-10-273-334-15
; Sequence 15, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

FILE REFERENCE: 031787.0076
CURRENT APPLICATION NUMBER: US/10/273,334
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US/05/591,500
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: PCT/US98/26433
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 60/069,677
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 895
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66)..(767)
OTHER INFORMATION:
US-10-273-334-15

Query Match 97.5%; Score 866.6; DB 6; Length 895;
Best Local Similarity 99.4%; Pred. No. 5.4e-173;
Matches 868; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	GGGTTGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGCGC	60
Db	1	GGGTTGCGGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGCGC	60
Qy	61	GAGAGATGGAGATGGGCGAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCCTCTGATG	120
Db	61	GAGAGATGGAGATGGGCGAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCCTCTGATG	120
Qy	121	TGAAGAACTTGCCTGGACACAGTCGGTCGATGAGGCAAACTCGAAGCCCTCACAG	180
Db	121	TGAAGAACTTGCCTGGACACAGTCGGTCGATGAGGCAAACTCGAAGCCCTCACAG	180
-Qy	181	ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG	240
Db	181	ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG	240
Qy	241	ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAAGCTTCTCTGCAACTCA	300
Db	241	ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAAGCTTCTCTGCAACTCA	300
Qy	301	TGGCAGAAAAGTGTCCAAACCTCAGGAGCTTCAAGTCTCAAGCTTCTCTGCAACTCA	360
Db	301	TGGCAGAAAAGTGTCCAAACCTCAGGAGCTTCAAGTCTCAAGCTTCTCTGCAACTCA	360
Qy	361	TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT	420
Db	361	TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT	420
Qy	421	CGGAGTTAACCACTGAACTGACGAGTACGAGAAACGTTCTCAAGCTTCTCTGCAACTCA	480
Db	421	CGGAGTTAACCACTGAACTGACGAGTACGAGAAACGTTCTCAAGCTTCTCTGCAACTCA	480
Qy	481	CATATCTCGACAGCTGTACTGGACCCACAGGAGGCCCTTACTCAGATATTGAGGACC	540
Db	481	CATATCTCGACAGCTGTACTGGACCCACAGGAGGCCCTTACTCAGATATTGAGGACC	540
Qy	541	ACGTGGAGGCCCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGAGTATGATGAAGATG	600
Db	541	ACGTGGAGGCCCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGAGTATGATGAAGATG	600
Qy	601	CTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGTGAAGAGGAGGAGC	660
Db	601	CTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGTGAAGAGGAGGAGC	660
Qy	661	TGAGTGGAGGGGACGAGGAGGATGAGAAAGGTTATTAACCATGGAGAGGTAGATGGCGAGG	720
Db	661	TGAGTGGAGGGGACGAGGAGGATGAGAAAGGTTATTAACCATGGAGAGGTAGATGGCGAGG	720

Qy	721	AAGATCAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAGAAAGCGAAAATGAGAACCTGAAG	780
Db	721	AAGATCAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAGAAAGCGAAAATGAGAACCTGAAG	780
Qy	781	ATGAGGGAAGAAGATGATGACTAAGTAGAATAACCTATTTTGAATAATTCCTATTGTGATT	840
Db	781	ATGAGGGAAGAAGATGATGACTAAGTAGAATAACCTATTTTGAATAATTCCTATTGTGATT	840
Qy	841	TGACTGTTTTTACCCCATATCCCTCCGCCCTCC 873	
Db	841	TGACTGTTTTTACCCCATATCCCTCCGCCCTCC 873	

RESULT 4

US-10-273-334-21
Sequence 21, Application US/10273334
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kochevar, Gerald J.
APPLICANT: Brody, Jonathan R.
APPLICANT: Kodkol, Shrihari S.
TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
FILE REFERENCE: 031787.0076
CURRENT APPLICATION NUMBER: US/10/273,334
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US/09/591,500
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: PCT/US98/26433
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 60/069,677
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 895
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66)..(767)
OTHER INFORMATION:
US-10-273-334-21

Query Match 97.3%; Score 865; DB 6; Length 895;
Best Local Similarity 99.3%; Pred. No. 1.2e-172;
Matches 867; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	GGGTTGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGCGC	60
Db	1	GGGTTGCGGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGCGC	60
Qy	61	GAGAGATGGAGATGGGCGAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCCTCTGATG	120
Db	61	GAGAGATGGAGATGGGCGAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCCTCTGATG	120
Qy	121	TGAAGAAGCTTCCCTGGACACACAGTCGGTCGATGAGGCAAACTCGAAGCCCTCACAG	180
Db	121	TGAAGAAGCTTCTCTGGACACACAGTCGGTCGATGAGGCAAACTCGAAGCCCTCACAG	180
Qy	181	ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG	240
Db	181	ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG	240
Qy	241	ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAAGGCGCCCTGGAAGTAT	300
Db	241	ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAAGGCGCCCTGGAAGTAT	300
Qy	301	TGGCAGAAAAGTGTCCAAACCTCAGGATCTATATTTAAGTGGCAACAAAATTAAGACC	360
Db	301	TGGCAGAAAAGTGTCCAAACCTCAGGATCTATATTTAAGTGGCAACAAAATTAAGACC	360
Qy	361	TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT	420

Db 361 TCAGCAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
Qy 421 GCGAGGTAAACCACTGACGACTACGAGAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Db 421 GCGAGGTAAACCACTGACGACTACGAGAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Qy 481 CATATCTCGACAGCTGTTACTGGGACCAACAGAGGCCCCCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACAGCTGTTACTGGGACCAACAGAGGCCCCCTTACTCAGATATTGAGGACC 540
Qy 541 ACGTGGAGGGCCTGGATGACAGAGAGAGGTTGAGCATGAGAGGAGTATGATGAAGATG 600
Db 541 ACGTGGAGGGCCTGGATGACAGAGAGAGGTTGAGCATGAGAGGAGTATGATGAAGATG 600
Qy 601 CTCAGGTAGTGAAGATGACGAGGCGGAGGAGGAGGAGGAGGTTGAAGAGGAGGAGC 660
Db 601 CTCAGGTAGTGAAGATGACGAGGCGGAGGAGGAGGAGGAGGAGGTTGAAGAGGAGGAGC 660
Qy 661 TCAGTGGAGGGGACGAGGAGGATGAAGAGGTTTAAACGATGAGAGGTTAGATGGCGAGG 720
Db 661 TCAGTGGAGGGGACGAGGAGGATGAAGAGGTTTAAACGATGAGAGGTTAGATGGCGAGG 720
Qy 721 AAGATGAAGAGAGCTGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 721 AAGATGAAGAGAGCTGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Qy 781 ATGAGGGAGAGAGATGATGACTAACTAGAACTATTTTGAAGAGGAGGAGGAGGAGGAGG 840
Db 781 ATGAGGGAGAGAGATGATGACTAACTAGAACTATTTTGAAGAGGAGGAGGAGGAGGAGG 840
Qy 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 873

RESULT 5
US-10-273-334-23
; Sequence 23, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273.334
; CURRENT FILING DATE: 2002-10-18
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-10-273-334-23

Query Match 94.4%; Score 839.4; DB 6; Length 895;
Best Local Similarity 97.5%; Pred. No. 2.7e-167;
Matches 851; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy 1 GGGTTCGAGGTTTATTGATGTAATTCGCTGGCAGAGAGGAGGCTCTGACAGACAGAGAGCGC 60
Db 1 GGGTTCGAGGTTTATTGATGTAATTCGCTGGCAGAGAGGAGGCTCTGACAGAGAGGAGCGC 60

Qy 61 GAGAGATGAGATGGGCAGACGATTCATTTCAGAGCTCGGAAACAGGCGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGGCAGACGATTCATTTCAGAGCTCGGAAACAGGCGCCCTCTGATG 120
Qy 121 TGAAGAAGCTTCCCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 121 TGAAGAAGCTTCCCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCACAG 180
Qy 181 ATGAATTTCAAGAAGCTTGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTCAAGAAGCTTGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Qy 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTGAGGCGGCTTGAAGTAT 300
Db 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTGAGGCGGCTTGAAGTAT 300
Qy 301 TGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAGTGGCAACAAAATTAAGAGCC 360
Db 301 TGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAGTGGCAACAAAATTAAGAGCC 360
Qy 361 TCAGCAACAATAGAGCCACTGAAACAGTTTAAAGAACTCAAGAGCTTAGACCTTTTCAATT 420
Db 361 TCAGCAACAATAGAGCCACTGAAACAGTTTAAAGAACTCAAGAGCTTAGACCTTTTCAATT 420
Qy 421 GCGAGTAAACCAACCTGAAACAGCTACGAGAGAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Db 421 GCGAGTAAACCAACCTGAAACAGCTACGAGAGAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Qy 481 CATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCGCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCGCTTACTCAGATATTGAGGACC 540
Qy 541 ACCTGAGGCGCTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
Db 541 ACCTGAGGCGCTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
Qy 601 CTCAGTGTGGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 601 CTCAGTGTGGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Qy 661 TGAGTGGAGGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 661 TGAGTGGAGGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Qy 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGAAAATGAGAACCTGGAAG 780
Db 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGAAAATGAGAACCTGGAAG 780
Qy 781 ATGAGGAGAGAAGATGATGACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTCGATT 840
Db 781 ATGAGGAGAGAAGATGATGACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTCGATT 840
Qy 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 873

RESULT 6
US-10-273-334-6
; Sequence 6, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273.334
; CURRENT FILING DATE: 2002-10-18
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-6

Query Match 93.5%; Score 831.4; DB 6; Length 907;
Best Local Similarity 97.4%; Pred. No. 1.3e-165;
Matches 883; Conservative 0; Mismatches 16; Indels 18; Gaps 3;

QY 1 GGGTTTCAGAGTTTATTCATTGAATTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGCGC 60
DB 1 GGGTTCGGGGTTATTGATGATTCGGCTGGCAGAGCCCTCTCAGACAGAGAGCGC 60

QY 61 GAGAGATGGAGATGGCGCAGACGGATTCAATTCAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120
DB 61 GAGAGCGGAGATGGCGCAGACGGATTCACTAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120

QY 121 TGAAGAAGCTTGCCTGGCAGACAGTCGGTCAATGAAGCAAACTCGAAGCCCTCACAG 180
DB 121 TGAAGAAGCTTGCCTGGCAGACAGTCGGTCAATGAAGCAAACTCGAAGCCCTCACAG 180

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCCTCACCTCAATCTCAG 240
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCCTCACCTCAATCTCAG 240

QY 241 ACTTACCAAAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 241 ACTTACCAAAAGTTAAGTGAAGCTTGAAGCAAACTCAACCTCAATCTCAG 240

QY 289 GCCTGGAAGTATGGCAGAAAGTCTTAAAGTAAATCAACGAGCGCCTCACCTCAATCTCAG 348
DB 289 GCCTGGAAGTATGGCAGAAAGTCTTAAAGTAAATCAACGAGCGCCTCACCTCAATCTCAG 348

QY 349 AAATTAAGAGCTTCAGCAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 360
DB 349 AAATTAAGAGCTTCAGCAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 360

QY 409 ACCTTTTCAATTCGAGGTTACCAACCTGAACGACTACGGAGAAACCGTGTTCAGAGCTTC 468
DB 409 ACCTTTTCAATTCGAGGTTACCAACCTGAACGACTACGGAGAAACCGTGTTCAGAGCTTC 468

QY 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCACAAAGGAGGAGGAGT 528
DB 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCACAAAGGAGGAGGAGT 528

QY 529 ATATTGAGGACCACTGGAGGGGCTGGATCAGCAGGAGGAGGCTGAGCATGAGGAGGAGT 588
DB 529 ATATTGAGGACCACTGGAGGGGCTGGATCAGCAGGAGGAGGCTGAGCATGAGGAGGAGT 588

QY 541 ATATTGAGGACCACTGGAGGGGCTGGATCAGCAGGAGGAGGCTGAGCATGAGGAGGAGT 600
DB 541 ATATTGAGGACCACTGGAGGGGCTGGATCAGCAGGAGGAGGCTGAGCATGAGGAGGAGT 600

QY 589 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 648
DB 589 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 648

QY 601 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 660
DB 601 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 660

QY 649 AAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATACCATGGAGAGG 708
DB 649 AAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATACCATGGAGAGG 708

QY 709 TAGATGGCAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGACGCAAAAT 768
DB 709 TAGATGGCAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGACGCAAAAT 768

QY 721 TAGATGGCAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGACGCAAAAT 780
DB 721 TAGATGGCAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGACGCAAAAT 780

QY 769 GAGAACTGAAGATGAGGAGGAGAGATGACTAAGTGAATACCTATTTTGAAGAAAT 828
DB 769 GAGAACTGAAGATGAGGAGGAGAGATGACTAAGTGAATACCTATTTTGAAGAAAT 828

QY 781 GAGAACTGAAGATGAGGAGGAGAGATGACTAAGTGAATACCTATTTTGAAGAAAT 840
DB 781 GAGAACTGAAGATGAGGAGGAGAGATGACTAAGTGAATACCTATTTTGAAGAAAT 840

QY 829 CCTATTGTGATTGACTGTTTACCATATCCCT-----CCCCCCTCAATCTGCC 882
DB 829 CCTATTGTGATTGACTGTTTACCATATCCCT-----CCCCCCTCAATCTGCC 882

QY 841 CCTATTGTGATTGACTGTTTACCATATCCCTCTCCGCCCCCTCTAATCTGCC 900
DB 841 CCTATTGTGATTGACTGTTTACCATATCCCTCTCCGCCCCCTCTAATCTGCC 900

QY 883 CCTGAA 889
DB 901 CCTGAA 907

RESULT 7
US-10-273-334-13
; Sequence 13, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-13

Query Match 85.8%; Score 762.6; DB 6; Length 907;
Best Local Similarity 92.6%; Pred. No. 3.5e-151;
Matches 840; Conservative 0; Mismatches 49; Indels 18; Gaps 3;

QY 1 GGGTTTCAGAGTTTATTCATTGAATTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGAGCGC 60
DB 1 GGGTTCGGGGTTATTGATGATTCGGCTGGCAGAGCCCTCTCAGAGAGAGAGCGC 60

QY 61 GAGAGATGGAGATGGCGCAGACGGATTCAATTCAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGCGCAGACGGATTCAATTCAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120

QY 121 TGAAGAAGCTTGCCTGGCAACAGTCGGTCAATGAAGCAAACTCGAAGCCCTCACAG 180
DB 121 TGAAGAAGCTTGCCTGGCAACAGTCGGTCAATGAAGCAAACTCGAAGCCCTCACAG 180

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCCTCACCTCAATCGCAA 240
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCCTCACCTCAATCGCAA 240

QY 241 ACTTACCAAAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 241 ACTTACCAAAAGTTAAGTGAAGCTTGAAGCAAACTCAACGATGAAGGAGTCTCAGGGG 300

QY 289 GCCTGGAAGTATGGCAGAAAGTCTTAAAGTAAATCAACGAGCGCCTCACCTCAATCTCAG 348
DB 289 GCCTGGAAGTATGGCAGAAAGTCTTAAAGTAAATCAACGAGCGCCTCACCTCAATCTCAG 348

QY 349 AAATTAAGAGCTTCAGCAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 360
DB 349 AAATTAAGAGCTTCAGCAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 360

QY 409 ACCTTTTCAATTCGAGGTTACCAACCTGAACGACTACGGAGAAACCGTGTTCAGAGCTTC 468
DB 409 ACCTTTTCAATTCGAGGTTACCAACCTGAACGACTACGGAGAAACCGTGTTCAGAGCTTC 468

QY 421 ACCTTTTCAATTCGAGGTTACCAACCTGAACGACTACGGAGAAACCGTGTTCAGAGCTTC 480
DB 421 ACCTTTTCAATTCGAGGTTACCAACCTGAACGACTACGGAGAAACCGTGTTCAGAGCTTC 480

QY 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCACAAAGGAGGAGGAGT 528
DB 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCACAAAGGAGGAGGAGT 528

Db 481 TCCGCAACTCACATATCTCGACGGCTATGACCGGGACGACAAGGAGGCCCTGACTCGG 540
Qy 529 ATATTGAGGACACGCTGGAGGGCTGGATGACGAGGAGGAGGGTGGATGAGGAGGAGT 588
Db 541 ATGCTGAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 600
Qy 589 ATGATGAGAGTCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 648
Db 601 ATGATGAGAGTCTCAGGTAGTGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
Qy 649 AAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATAAGATGGAGAGG 708
Db 661 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGATGAAGAGGTTATAAGATGGAGAGG 720
Qy 709 TAGATGGCGAGGAGATCAAGACAGCTTGGTGAAGAGAAAGGGTCAGACGGAAT 768
Db 721 TAGATGAGGAGGAGATGAAGAGGCTTGGTGAAGAGAAAGGGTCAGACGGAAT 780
Qy 769 GAGAACCTGAAGATGAGGAGGAGGAGATGACTAAGTAGAATAACCTATTTGAAAAAT 828
Db 781 GAGAACCTGAAGATGAGGAGGAGGAGATGACTAAGTAGAATAACCTATTTGAAAAAT 840
Qy 829 CCTATTGATTTGACTGTTTTTACCATATCCCT-----CCCCCTCCATCTCTGCC 882
Db 841 CCTATTGATTTGACTGTTTTTACCATATCCCTCTCCCCCTCTCTAATCTCTGCC 900
Qy 883 CCCTGAA 889
Db 901 CCCTGAA 907

RESULT 8

US-10-273-334-25
; Sequence 25, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-25

Query Match 85.6%; Score 761; DB 6; Length 907;
Best Local Similarity 92.5%; Pred. No. 7.5e-151;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTTGAATTCGGCTGGCAGGAGGCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGAGGTTTATTGATTTGAATTCGGCTGGCAGGAGGCTCTGCAGACAGAGAGCGC 60
Qy 61 GAGAGATGAGATGGCAGACGATTCATTTCAGAGCTCGGAAACAGAGCGGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGCAGACGATTCATTTCAGAGCTCGGAAACAGAGCGGCCCTCTGATG 120
Qy 121 TGAAGAAGACTTCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 121 TGAAGAAGACTTCTCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGGCGCTCACAG 180

Qy 181 ATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACGAGGCGCTACCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACGAGGCGCTACCTCAATCTCAG 240
Qy 241 ACTTACCAAGTTA--AAGTTGAGAAAGCTTGAACCT-----AGAGTCTCAGGG 288
Db 241 ACTTACCAAGTTA--AAGTTGAGAAAGCTTGAACCT-----AGAGTCTCAGGG 300
Qy 289 GCTTGAAGTATTGGCAGAAAAGTGTCCAAAGCTCAGCATCTATATTTAAGTGGCAACA 348
Db 301 GCTTGAAGTATTGGCAGAAAAGTGTCCAAAGCTCAGCATCTATATTTAAGTGGCAACA 360
Qy 349 AAATTAAGACCTTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 361 AAATTAAGACCTTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 420
Qy 409 ACCTTTTCAATTTGCGAGGTAAACCACTGAGCACTACGAGGAGGAGGAGGAGGAGGAGT 468
Db 421 ACCTTTTCAATTTGCGAGGTAAACCACTGAGCACTACGAGGAGGAGGAGGAGGAGGAGT 480
Qy 469 TCTTCAACTCATATCTCGACAGCTGTACTGGGACCAAGAGGAGGAGGAGGAGGAGGAGT 528
Db 481 TCCGCAACTCACATCTCGACGGCTATGACGGGCTATGACGGGACGACAAAGGAGGAGGAGT 540
Qy 529 ATATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 588
Db 541 ATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 600
Qy 589 ATGATGAAGATCTCAGGTAGTGGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 648
Db 601 ATGATGAAGATCTCAGGTAGTGGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
Qy 649 AAGAGGAGGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
Db 661 AAGAGGAGGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 720
Qy 709 TAGATGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 768
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RESULT 9

US-10-273-334-33
; Sequence 33, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn version 3.1

SEQ ID NO 33

LENGTH: 906

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (66)..(812)

OTHER INFORMATION:

US-10-273-334-33

Query Match 85.5%; Score 760.2; DB 6; Length 906;
Best Local Similarity 93.2%; Pred. No. 1.1e-150;
Matches 845; Conservative 0; Mismatches 43; Indels 19; Gaps 4;

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Db 900 CCCTGAA 906

RESULT 10

US-10-273-334-28

Sequence 28, Application US/10273334

GENERAL INFORMATION:

APPLICANT: Pasternack, Gary R.

APPLICANT: Kochevar, Gerald J.

APPLICANT: Brody, Jonathan R.

APPLICANT: Kodkol, Shrihari S.

TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

FILE REFERENCE: 031787.0076

CURRENT APPLICATION NUMBER: US/10/273,334

CURRENT FILING DATE: 2002-10-18

PRIOR APPLICATION NUMBER: US/09/591,500

PRIOR FILING DATE: 2000-12-06

PRIOR APPLICATION NUMBER: PCT/US98/26433

PRIOR FILING DATE: 1998-12-11

PRIOR APPLICATION NUMBER: US 60/069,677

PRIOR FILING DATE: 1997-12-11

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn version 3.1

SEQ ID NO 28

LENGTH: 907

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (66)..(812)

OTHER INFORMATION:

US-10-273-334-28

Query Match

Best Local Similarity 85.2%; Score 757.8; DB 6; Length 907;

Mismatches 837; Conservative 0; Mismatches 52; Indels 18; Gaps 3;

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Db 61 GAGAGATGAGATGGCAGACGGATTTCATTCAGAGCTGCGGAACAGGCGCCCTCTGATG 120
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Db 121 TGAAGAAGTTCGCTCGACAAACAGTCGTCGATGAAGGCAAACTCGAAGGCGCTCACAG 180
QY 181 ATGAATTTGAAGAAGTTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAAGTTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
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; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(810)
; OTHER INFORMATION:
US-10-273-334-11

Query Match      80.1%; Score 711.8; DB 6; Length 905;
Best Local Similarity 90.2%; Pred. No. 1.6e-140;
Matches 798; Conservative 0; Mismatches 73; Indels 14; Gaps 3;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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3	857.8	94.6	905	22	US-09-591-500-19	Sequence 19, Appl
4	857.8	94.6	905	22	US-09-591-500-26	Sequence 26, Appl
5	856.2	94.4	905	22	US-09-591-500-7	Sequence 7, Appli
6	833.4	91.9	907	22	US-09-591-500-9	Sequence 9, Appli
7	827.8	91.3	906	22	US-09-591-500-33	Sequence 33, Appl
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15	822.2	90.7	907	22	US-09-591-500-28	Sequence 28, Appl
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17	822.2	90.7	1197	42	US-10-216-583-94	Sequence 94, Appl
18	822.2	90.7	1595	25	US-09-644-871-8887	Sequence 8887, Ap
19	822.2	90.7	1595	25	US-09-644-871-8887	Sequence 8887, Ap
20	822.2	90.7	1595	25	US-09-652-913-10130	Sequence 10130, A
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LOCATION: (66)..(455)
OTHER INFORMATION:
US-09-591-500-30

Query Match 97.5%; Score 884.6; DB 22; Length 907;
Best Local Similarity 98.5%; Pred. No. 1.3e-164;
Matches 893; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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QY 241 ACTTACCAAAAGTTAAACAACTTAAAGAGCTTGAAGCTTAAGCACTCAAGCTCAAGTGG 300
DB 241 ACTTACCAAAAGTTAAACAACTTAAAGAGCTTGAAGCTTGAAGCTCAAGTGG 300

QY 301 GCCTAGAAGTATTGGCAAGAAAGTGTCCAAACCTCATACATCAATTTAAGTGGCAACA 360
DB 301 GCCTAGAAGTATTGGCAAGAAAGTGTCCAAACCTCATACATCAATTTAAGTGGCAACA 360

QY 361 AAATTAAGAACTCAGCACATAGAGCCCTGAAAGCTTGAAGAACTTGAAGAACTTGAAG 420
DB 361 AAATTAAGAACTCAGCACATAGAGCCCTGAAAGCTTGAAGAACTTGAAGAACTTGAAG 420

QY 421 ACCTTTTCACTTGGAGGTAAACCACTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
DB 421 ACCTTTTCACTTGGAGGTAAACCACTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480

QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGGATGACAGAGGCGCCCTAACTCGG 540
DB 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGGATGACAGAGGCGCCCTAACTCGG 540

QY 541 ATGGTGAGGGCTTTGTGGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600
DB 541 ATGGTGAGGGCTTTGTGGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600

QY 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
DB 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT 660

QY 661 AAGAGGAGGAGCTGAGTGGAGACGAGAGAGAGATGAGGATGAGGATGAGGATGAGGAGG 720
DB 661 AAGAGGAGGAGCTGAGTGGAGACGAGAGAGAGATGAGGATGAGGATGAGGATGAGGAGG 720

QY 721 TAGATGATGAGGAGATGAGGAGAGCTTGGTGAAGAAAGAGGGTCAAGAGCGGAAAT 780
DB 721 TAGATGATGAGGAGATGAGGAGAGCTTGGTGAAGAAAGAGGGTCAAGAGCGGAAAT 780

QY 781 AAGAACTGAAGATGAGGAGAGACGATGCCCTAAGTGGAAATATCTATTTTGAAGAAAT 840
DB 781 AAGAACTGAAGATGAGGAGAGACGATGCCCTAAGTGGAAATATCTATTTTGAAGAAAT 840

QY 841 CCTTTCTGATTTTACTGTTTTTACCGGTACCCCTCTCCCCCCCCACCTCAATCTCTGCC 900
DB 841 CCTATTGTGATTTGACTGTTTTTACCCTATCCCTCTCCCCCCCCCTCTCAATCTCTGCC 900

QY 901 CCCTGAA 907
DB 901 CCCTGAA 907

RESULT 3
US-09-591-500-19
; Sequence 19, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(453)
; OTHER INFORMATION:
US-09-591-500-19

Query Match 94.6%; Score 857.8; DB 22; Length 905;
Best Local Similarity 97.4%; Pred. No. 2.6e-159;
Matches 883; Conservative 0; Mismatches 22; Indels 2; Gaps 1;

QY 1 GGGTTCGGGGTTTATTGATGAATTCGGCTGGCGGGAGCCTCTGCAGAGAGAGCGC 60
DB 1 GGGTTCGGGGTTTATTGATGAATTCGGCTGGCGGGAGCCTCTGCAGAGAGAGCGT 58

QY 61 GAGAGATGAGATGGGACGACGATTCATTTAGAGCTGCGGAACGGGAGCGCCCTCTGATG 120
DB 59 GAGAGATGAGATGGGACGACGATTCATTTAGAGCTGCGGAACGGGAGCGCCCTCGATG 118

QY 121 TGAAGAACTTGTCTTGGACAACTGCGGTGGAATGAAGGCAAACTCGAAGGCGCTCACAG 180
DB 119 TGAAGAACTTGTCTTGGACAACTGCGGTGGAATGAAGGCAAACTCGAAGGCGCTCACAG 178

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGCTAGGCTCACTCAATCGCAA 240
DB 179 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGCTAGGCTCACTCAATCGCAA 238

QY 241 ACTTACCAAAAGTTAAACAACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 300
DB 239 ACTTACCAAAAGTTAAACAACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 298

QY 301 GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
DB 299 GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 358

QY 361 AAATTAAGAACTCAGCACAACTAGAGCCCTGAAAAAGTTAGAAAACTTCGAGAGCTTAG 420
DB 359 AAATTAAGAACTCAGCACAACTAGAGCCCTGAAAAAGTTAGAAAACTTCGAGAGCTTAG 418

QY 421 ACCTTTTCACTTGGCAGGTAAACCACTGGAACAACTTACTGAGAGAGATGTTCAAGCTCC 480
DB 419 ACCTTTTCACTTGGCAGGTAAACCACTGGAACAACTTACTGAGAGAGATGTTCAAGCTCC 478

QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGGATGACAGAGGCGCCCTAACTCGG 540
DB 479 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGGATGACAGAGGCGCCCTAACTCGG 538

QY 541 ATGGTGAGGGCTTTGTGGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600
DB 539 ATGGTGAGGGCTTTGTGGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 598

QY 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT 660

OTHER INFORMATION:

US-09-591-500-7

Query Match 94.4%; Score 856.2; DB 22; Length 905;
Best Local Similarity 97.2%; Pred. No. 5.3e-159;
Matches 882; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGGAGCCTCTGCAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGGAGCCTCTGCAGAGAGAGCGT 58
Qy 61 GAGAGATGAGATGGCAGACGAGTTCATTTAGAGCTCGGGAACGGAGCGCCTCTGATG 120
Db 59 GAGAGATGAGATGGCAATGAGTTCATTTAGAGCTCGGGAACGGAGCGCCTCTGATG 118
Qy 121 TGAAGAACTTTCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGGCTCAG 180
Db 119 TGAAGAACTTTCCTGGACACAGTCAGTCAATGAAGGCAAACTTGAAGGCTCAG 178
Qy 181 ATGAATTTGAAGAACTTGAATTCATTAAGTACAATCAACGTAGGCTCACTCAATCGCA 240
Db 179 ATGAATTTGAAGAACTTGAATTCATTAATCAATCAATAGGCTCACCTCAATTCGA 238
Qy 241 ACTTACCAAGCTTAACAACTTAAGAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG 300
Db 239 ACTTACCAAGCTTAACAACTTAAGAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG 298
Qy 301 GCCTAGAGATTTGGCAGAAAGTGTCCAACTCATACTACATCTAAATTTAAGTGGCAACA 360
Db 299 GCCTAGAGATTTGGCAGAAAGTGTCCAACTCATACTACATCTAAATTTAAGTGGCAACA 358
Qy 361 AAATTAAGAGCTCAGCACAAATAGAGCCCTGAAAGAGTTAGAAACCTCGAGAGCTTAG 420
Db 359 AAATTAAGAGCTCAGCACAAATAGAGCCCTGAAAGAGTTAGAAACCTCGAGAGCTTAG 418
Qy 421 ACCTTTTCACTTGGAGGTAAACAACTGAACTACTGAGAAAGATGTTCAAGCTCC 480
Db 419 ACCTTTTCACTTGGAGGTAAACAACTGAACTACTGAGAAAGATGTTCAAGCTCC 478
Qy 481 TCCCTGCAACTCACAATCTCAAGGCTGTGACCCGGATGACAGAGGAGGCGCCCTAACTCGG 540
Db 479 TCCCTGCAACTCACAATCTCAAGGCTGTGACCCGGATGACAGAGGAGGCGCCCTAACTCGG 538
Qy 541 ATGCTGAGGCTTTGTGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGGAGT 600
Db 539 ATGCTGAGGCTTTGTGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGGAGT 598
Qy 601 ATGATGAAGATGCTCAGGTAAATGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db 599 ATGATGAAGATGCTCAGGTAAATGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT 658
Qy 661 AAGAGGAGGAGGAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 659 AAGAGGAGGAGGAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 718
Qy 721 TAGATGATGAGGAGGAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 719 TAGATGATGAGGAGGAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 778
Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Db 779 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 838
Qy 841 CCTTTTGTGATTTTACTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTG 900
Db 839 CCTTTTGTGATTTTACTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTG 898
Qy 901 CCTGAA 907
Db 899 CCTGAA 905

RESULT 6

US-09-591-500-9

; Sequence 9, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-09-591-500-9

Query Match 91.9%; Score 833.4; DB 22; Length 907;
Best Local Similarity 94.9%; Pred. No. 1.7e-154;
Matches 861; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGGAGCCTCTGCAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGGAGCCTCTGCAGAGAGAGCGC 60
Qy 61 GAGAGATGAGATGGCAGACGAGTTCATTTAGAGCTCGGGAACGGAGCGCCTCTGATG 120
Db 61 GAGAGATGAGATGGCAGACGAGTTCATTTAGAGCTCGGGAACGGAGCGCCTCTGATG 120
Qy 121 TGAAGAACTTTCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGGCTCAGAC 180
Db 121 TGAAGAACTTTCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGGCTCAGAC 180
Qy 181 ATCAATTTGAAGAACTTGAATTCATTAAGTACAATCAAGTAGGCTCAGCTCAATCGCA 240
Db 181 ATCAATTTGAAGAACTTGAATTCATTAAGTACAATCAAGTAGGCTCAGCTCAATCGCA 240
Qy 241 ACTTACCAAGTAAACAACTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGA 300
Db 241 ACTTACCAAGTAAACAACTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGA 300
Qy 301 GCCTGAGAGTATGGCAGAAAGTGTCCAAAGCTCATACATCTAAATTTAAGTGGCAACA 360
Db 301 GCCTGAGAGTATGGCAGAAAGTGTCCAAAGCTCATACATCTAAATTTAAGTGGCAACA 360
Qy 361 AAATTAAGAGCTCAGCAATAGAGCCCTGAAAAGTTAGAAAACCTCGAAGGCTTAG 420
Db 361 AAATTAAGAGCTCAGCAATAGAGCCCTGAAAAGTTAGAAAACCTCGAAGGCTTAG 420
Qy 421 ACCTTTTCACTTGGAGGTAAACAACTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAG 480
Db 421 ACCTTTTCACTTGGAGGTAAACAACTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAG 480
Qy 481 TCCTGCAACTCACAATCTCAAGGCTGTGACCCGGATGACAAAGGAGGCGCCCTAACTCGG 540
Db 481 TCCTGCAACTCACAATCTCAAGGCTGTGACCCGGATGACAAAGGAGGCGCCCTAACTCGG 540
Qy 541 ATGCTGAGGCTTTCTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGAGGAGT 600
Db 541 ATGCTGAGGCTTTCTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGAGGAGT 600
Qy 601 ATGATGAAGATGCTCAGGTAAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGGTAAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660


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Db 601 ATGATGAAGATGCTCAGGTAGTAGAAGATGAGGAGGAGGAGGATCAGGAGGAGGAAGGTG 660
Qy 661 AGAGGAGGACCTGAGTGGAGCAGGAGGAGGAGGATGAAGGTATATAACAATGAGAGG 720
Db 661 AGAGGAGGACCTGAGTGGAGGAGGAGGAGGAGGATGAAGGTATATAACAATGAGAGG 720
Qy 721 TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGCAAAAT 780
Db 721 TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGCAAAAT 780
Qy 781 AGAAACCTGAAGATGAGGAGGAGGAGGATGCTTAAGTGAATATCTATTTTGAATAAT 840
Db 781 GAGAACTGAAGATGAGGAGGAGGAGGATGCTTAAGTGAATATCTATTTTGAATAAT 840
Qy 841 CCTTTTGTGATTTACTGTTTTTACCGTACCCCTCTCCCGCCCTCTAATCCTGCC 900
Db 841 CCTATTGTGATTGACTGTTTTTACCCTATCCCTCTCCCGCCCTCTAATCCTGCC 900
Qy 901 CCCTGAA 907
Db 901 CCCTGAA 907

RESULT 7
US-09-591-500-33
; Sequence 33, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-09-591-500-33

Query Match 91.3%; Score 827.8; DB 22; Length 906;
Best Local Similarity 95.3%; Pred No. 2.2e-153;
Matches 864; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

Qy 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGGAGCCTCTGAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGGAGCCTCTGAGAGAGAGAGCGC 60
Qy 61 GAGAGATGAGATGGGAGAGAGGATTCATTTAGAGTGGGAGGAGCGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGGAGAGAGGATTCATTTAGAGTGGGAGGAGCGCCCTCTGATG 120
Qy 121 TGAAGAAGCTTTCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGGCTTCACAG 180
Db 121 TGAAGAAGCTTTCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGGCTTCACAG 180
Qy 181 ATGAATTGAAGAACTGGAATCTTAAGTACAATCAACGTAGCGCTCACTCAATCGCAA 240
Db 181 ATGAATTGAAGAACTGGAATCTTAAGTACAATCAACGTAGCGCTCACTCAATCGCAA 240
Qy 241 ACTTACCAAGTTAAACAACCTTAAGAACTTAAGCAAGTAACAGAGCTCAGTGG 300
Db 241 ACTTACCAAGTTAAACAACCTTAAGAACTTAAGCAAGTAACAGAGCTCAGTGG 300
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Db 241 ACTTACCAAGTTAAACAACCTTAAGAACTTAAGCAAGTAACAGAGCTCAGGCG 300
Qy 301 GCCTAGAACTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAAGTGGCAACA 360
Db 301 GCCTAGAACTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAAGTGGCAACA 360
Qy 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAAACCTCAAGAGCTTAG 420
Db 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAAACCTCAAGAGCTTAG 420
Qy 421 ACCTTTTCACCTTCGGAGGTAAACCAACCTGAACAACCTACTGAGAGAGAGATGTTCAACCTCC 480
Db 421 ACCTTTTCACCTTCGGAGGTAAACCAACCTGAACAACCTACTGAGAGAGAGATGTTCAACCTCC 480
Qy 481 TCCTGCAACTCACAATATCTCAACGGCTGTGACCCGGGTGACAAAGGAGGCGCCCTAACTCGS 540
Db 481 TCCTGCAACTCACAATATCTCAACGGCTGTGACCCGGGTGACAAAGGAGGCGCCCTAACTCGS 540
Qy 541 ATGCTGAGGCGCTTGTGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 541 ATGCTGAGGCGCTTGTGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
Qy 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660
Qy 661 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGGTTATAACAATGGAGAGG 720
Db 661 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGGTTATAACAATGGAGAGG 720
Qy 721 TAGATGATGAGGAAGATGAACAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGAGGAGG 780
Db 721 TAGATGATGAGGAAGATGAACAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGAGGAGG 780
Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGATGCCTAAGTGAATATCTATTTTGAATAAT 840
Db 780 GAGAACTGAAGATGAGGAGGAGGAGGAGGATGCCTAAGTGAATATCTATTTTGAATAAT 840
Qy 841 CCTTTTGTGATTTACTGTTTTTACCGCTACCCCTCTCCCGCCCTCTAATCCTGCC 900
Db 840 CCTATTGTGATTGACTGTTTTTACCCTATCCCTCTCCCGCCCTCTAATCCTGCC 899
Qy 901 CCCTGAA 907
Db 900 CCCTGAA 906

RESULT 8
PCT-US02-25766-3866
; Sequence 3866, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E.
; APPLICANT: FAULK, Ronald
; APPLICANT: SUN, Hongwei
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3866
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U73477
PCT-US02-25766-3866
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Query Match				91.0%	Score 825.4;	DB 1;	Length 1052;
Best Local Similarity				94.4%;	Pred. No. 6.6e-153;		
Matches 856; Conservative				0;	Mismatches 51;	Indels	0;
QY	1	GGGTCGGGGTTTATTCATTTCAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGAGCGC	60				
Db	32	GGGTCGGGGTTTATTCATTTCAATTCGGCGGGAGCCCTCTGCAGAGAGAGAGCGC	91				
QY	61	GAGAGATGGAGATGGGCAGACGGATTCATTTAGAGCTGCGGAACGGGACGCCCTCTTGATG	120				
Db	92	GAGAGATGGAGATGGGCAGACGGATTCATTTAGAGCTGCGGAACGGGACGCCCTCTTGATG	151				
QY	121	TGAAGAAGACTTGTCTCTGGACACAGTCGCTGGAATGAAGCAACCTCGAAGGCCCTCACAG	180				
Db	152	TGAAGAAGACTTGTCTCTGGACACAGTCGCTGGAATGAAGCAACCTCGAAGGCCCTCACAG	211				
QY	181	ATGAATTTGAAGAACTCGAATTCCTTAAGTACAATCAAGCTAGGCCCTCACTCAATCGCAA	240				
Db	212	ATGAATTTGAAGAACTCGAATTCCTTAAGTACAATCAAGCTAGGCCCTCACTCAATCGCAA	271				
QY	241	ACTTTACCAAGTTTAAACAAACTTTAAGAAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG	300				
Db	272	ACTTTACCAAGTTTAAACAAACTTTAAGAAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG	331				
QY	301	GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	360				
Db	332	GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	391				
QY	361	AAATTTAAGACCTTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG	420				
Db	392	AAATTTAAGACCTTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG	451				
QY	421	ACCTTTTCACTTCGGAGGTAAACCAACCTGAACAACTACTGAGAGAAGATGTTCAAGCTCC	480				
Db	452	ACCTTTTCAATTCGGAGGTAAACCAACCTGAACAACTACCAGAGAAATGTGTTCAAGCTCC	511				
QY	481	TCCTGCAACTTCACATATCTCAACGCTGTGACCCCGATGACANGAGGCCCCCTAACTCGG	540				
Db	512	TCCGCAACTTCACATATCTCGACGGCTATGACCGGACCAAGGAGGCCCTTGACTCGG	571				
QY	541	ATGGTGAGGCGCTTTGTGGAGTCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGAGT	600				
Db	572	ATGCTGAGGCGCTACGTGGAGGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	631				
QY	601	ATGATGAAGATGCTCAGGTTAATGGAAAGATGAGGAGCAACGAGGATGAGGAGGAGGAACGTG	660				
Db	632	ATGATGAAGATGCTCAGGTTAGTGAAGACGAGGAGGACGAGGATGAGGAGGAGGAAGGTG	691				
QY	661	AAAGAGGAGACGTGAGTGGAGACGAGGAGGAGAGGATCAAGGTTATAACAATGGAGAGG	720				
Db	692	AAAGAGGAGACGTGAGTGGAGAGGAGAGAGGATGAAGAAGTTATAACGATGGAGAGG	751				
QY	721	TAGATGATGAGGAAGATGAAGAAGACTTGGTGAAGAAGAAAGGGGTCAAGAAGCGAAAT	780				
Db	752	TAGATGACGAGGAAGATGAAGAAGACTTGGTGAAGAAGAAAGGGGTCAAGAAGCGAAAC	811				
QY	781	AAGAACTGAAGATGAGGAGAGACGATGCCCTAAGTGGAAATAATCTATTTTGAATAAT	840				
Db	812	GAGAAGCTGAAGATGAGGAGAGAGATGATGACTAAGTGGAAATAACCTATTTTGAATAAT	871				
QY	841	CTTTTGTGATTTTACTGTTTTTATAGCCGTACCCCTCTCCCGCCACCTCAATCCTCGC	900				
Db	872	CCTATTGTGATTTGACTGTTTTTACCCTATCCTCTCTCCCGCCCTCTCAATCCTCGC	931				
QY	901	CCCTGAA	907				
Db	932	CCCTGAA	938				

RESULT 9
US-09-205-070-14975
; Sequence 14975, Application US/09205070

```

: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
: TITLE OF INVENTION: LIBRARIES
: FILE REFERENCE: 20411-748
: CURRENT APPLICATION NUMBER: US/09/205,070
: CURRENT FILING DATE: 1998-12-03
: NUMBER OF SEQ ID NOS: 45207
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 14975
: LENGTH: 2398
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-205-070-14975

```

Query Match 91.0%; Score 825.4; DB 16; Length 2398;
Best Local Similarity 94.4%; Pred. No. 7.6e-153;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY	1	GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGCGGAGCCCTCTCGAGAGAGAGCGC	60
Db	32	GGGTTTCGGGGTTTATTGATTGAATTCGGCGCGGAGCCCTCTCGAGAGAGAGCGC	91
QY	61	GAGAGATGGAGATGGCGACGCGGATTTCATTTAGAGCTGCGGAACGGAGCGCCTCTGATG	120
Db	92	GAGAGATGGAGATGGCGACGCGGATTTCATTTAGAGCTGCGGAACGGAGCGCCTCTGATG	151
QY	121	TGAAGAACAATGTCCTGGACACAGTCGGTCGAATCAAGGCCAACTCGAAGGCCCTCACAG	180
Db	152	TGAAGAGACTGTCCTGGACACAGTCGGTCGAATGAAGCCAACTCGAAGGCCCTCACAG	211
QY	181	ATGAATTTGAAGAACCTGGAATCTTTAAGTACAATCAACCTAGCGCTCACTCAATCGCAA	240
Db	212	ATGAATTTGAAGAACCTGGAATCTTTAAGTACAATCAACCTAGCGCTCACTCAATCGCAA	271
QY	241	ACTTACCAAGTTTAAACAACCTTGAAGACTTTGAATCAAGAGCTTAACGAGCGCTCAGTGG	300
Db	272	ACTTACCAAGTTTAAACAACCTTGAAGACTTTGAATCAAGAGCTTAACGAGCTCAGGGG	331
QY	301	GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTTAATTTAACTGCGCAACA	360
Db	332	GCCTAGAAGTATTGGCAGAAAAGTGTCCGAACCCTACGCATCTTAATTTAAGTGGCAACA	391
QY	361	AAATTTAAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG	420
Db	392	AAATTTAAAGACCTCAGCACAAATAGAGCCACTGAAAAGTTAGAAAACCTCAAGAGCTTAG	451
QY	421	ACCTTTTCACTTCCGAGGTTAACCAACCTGAACAACCTACTGAGAGAAGATGTTTCAAGCTCC	480
Db	452	ACCTTTTCAATTCGCGAGGTAAACCAACCTGAACGACTACCGAGAAAATGTGTTCAAGCTCC	511
QY	481	TTCCTCAACTCACATATCTCAACGGCTGTGCCCGATCACAGGAGGCCCTCAACTCGG	540
Db	512	TCCCGCACTCACATATCTCGAGGGTATGACCGGGACACAAGGAGGCCCTGACTCGG	571
QY	541	ATGGTGAGGGCTTTGTGGAGTGCGCTGGATGCAAGGAGGAGGATGAGGTAGGAGGAGT	600
Db	572	ATGCTCAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGTAGGAGGAGT	631
QY	601	ATGATGAAGATGCTCAGGTTAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGAACCTG	660
Db	632	ATGATGAAGATGCTCAGGTTAGTGGAAAGACGAGGAGGACGAGGATGAGGAGGAGGAGT	691
QY	661	AAGAGGAGACGTGAGTGGAGACGAGGAGGAAGGATCAAGGTTATACATGAGGAGG	720
Db	692	AAGAGGAGACGTGAGTGGAGAGGAGGAGGAGGATGAAGAGGTTATACGATGAGGAGG	751
QY	721	TAGATGATGAGGAAGATGAAGAAGACTTGGTGAAGAAGAAAAGGGGTCAAGAAGCGAAAT	780
Db	752	TAGATGACGAGGAGATGAAGAGACTTGGTGAAGAAGAAAAGGGGTCAAGAAGCGAAAC	811
QY	781	AGAAACTGAAGATGAGGAGAGACGATGCCTTAAGTGAATTAATCTATTTTGAATAATT	840

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Db 812 GAGAACTGAAGATGAGGAGGAAGATGATGACTAAGTGAATAACCAATATTTTGAATAATT 871
QY 841 CTTTTGTGATTTACTCTTTTAGCCGTACCCCTCTCCGCCCCCACTCTAATCTCTGCC 900
Db 872 CCTATTGTGATTTGACTGTTTTTACCCATATCCCTCTCCGCCCCCACTCTAATCTCTGCC 931
QY 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 10
US-09-340-623-14975
; Sequence 14975, Application US/09340623
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/340,623
; CURRENT FILING DATE: 1999-06-28
; EARLIER APPLICATION NUMBER: US 09/205,070
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14975
; LENGTH: 2398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-340-623-14975

Query Match 91.0%; Score 825.4; DB 17; Length 2398;
Best Local Similarity 94.4%; Pred. No. 7.6e-153;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTGCGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGAGCCCTGCGAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCGAGACGGATTCATTTAGAGCTGCGGAACGGAGCGCCTCTGATG 120
Db 92 GAGAGATGAGATGGCGAGACGGATTCATTTAGAGCTGCGGAACGGAGCGCCTCTGATG 151
QY 121 TGAAGAAGCTTCTCTGGACAACTGCGTGAATGAAGCAAACTCGAAGGCTTCACAG 180
Db 152 TGAAGAAGCTTCTCTGGACAACTGCGTGAATGAAGCAAACTCGAAGGCTTCACAG 211
QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAACGTAGGCCTCACCTCAATCGCAA 240
Db 212 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAACGTAGGCCTCACCTCAATCGCAA 271
QY 241 GCGTAGAAGTATTGGCAGAAAAGTGTCGCAAACTCATACATCTAATTTAAGTGGCAACA 360
Db 332 GCGTAGAAGTATTGGCAGAAAAGTGTCGCAAACTCATACATCTAATTTAAGTGGCAACA 391
QY 361 AATTTAAGACCTTCAGCAAACTAGAGCCCTGAAAGAGTTAGAAAACCTTCGAGAGCTTAG 420
Db 392 AATTTAAGACCTTCAGCAAACTAGAGCCCTGAAAGAGTTAGAAAACCTTCGAGAGCTTAG 451
QY 421 ACCTTTTCACTTCGAGAGTAACTCAACCTGAACAACTACTGAGAGAGAGATGTTTCAAGCTCC 480
Db 452 ACCTTTTCACTTCGAGAGTAACTCAACCTGAACAACTACTGAGAGAGATGTTTCAAGCTCC 511
QY 481 TCCTGCAACTACATATCTCAAGGGCTGTGACCCGGATGACAGAGGCGCCCTACTCGG 540
Db 512 TCCTGCAACTACATATCTCAAGGGCTGTGACCCGGATGACAGAGGCGCCCTACTCGG 571
QY 541 ATGGTGAAGGCTTTGTGGAGTGCCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600
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Db 572 ATCCTGAGGCTTACGTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631
QY 601 ATGATGAAGATGCTCAGGTAATCGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db 632 ATGATGAAGATGCTCAGGTAATCGAAGATGAGGAGGAGGAGGAGGATGAGGAGGAGGAGT 691
QY 661 AAGAGGAGGACGTGAGTGGAGAGGAGGAGGAGGATGAAGGTTATACATTTGAGAGG 720
Db 692 AAGAGGAGGACGTGAGTGGAGAGGAGGAGGAGGATGAAGGTTATACATTTGAGAGG 751
QY 721 TAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAAGAGGGTTCAGAACGCGAAAT 780
Db 752 TAGATGAGGAGGAAGATGAAGAGAGCTTGGTGAAGAAGAGGGTTCAGAACGCGAAAT 811
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGATGCCTTAAGTGAATAATCTATTTTGAATAAT 840
Db 812 GAGAACTGAAGATGAGGAGGAGGAGGATGCCTTAAGTGAATAATCTATTTTGAATAAT 871
QY 841 CCTTTGTGATTTTACTGTTTTTGGCGGTACCCCTCTCCGCCCCCACTCTAATCTCTGCC 900
Db 872 CCTATTGTGATTTGACTGTTTTTACCATATCCCTCTCCGCCCCCACTCTAATCTCTGCC 931
QY 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 11
US-09-898-888-14975
; Sequence 14975, Application US/09898888
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/898,888
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/340,623
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14975
; LENGTH: 2398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-888-14975

Query Match 91.0%; Score 825.4; DB 33; Length 2398;
Best Local Similarity 94.4%; Pred. No. 7.6e-153;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTGCGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGAGCCCTGCGAGAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCGAGCGGATTCATTTAGAGCTGCGGAACGGAGCGCCTCTGATG 120
Db 92 GAGAGATGAGATGGCGAGCGGATTCATTTAGAGCTGCGGAACGGAGCGCCTCTGATG 151
QY 121 TGAAGAAGCTTCTCTGGACAACTGCGTGAATGAAGCAAACTCGAAGGCTTCACAG 180
Db 152 TGAAGAAGCTTCTCTGGACAACTGCGTGAATGAAGCAAACTCGAAGGCTTCACAG 211
QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAACGTAGGCCTCACCTCAATCGCAA 240
Db 212 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAACGTAGGCCTCACCTCAATCGCAA 271
QY 241 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGG 300
Db 272 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTAAGCAGTAACAGAGCTCAGTGG 331
QY 301 GCCTAGAGTATTGGCAGAAAAGTGTCGCAAACTCATACATCTAATTTAAGTGGCAACA 360
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Db 332 GCCTAGAGTATTGGCAGAAAAGTGTCCGAACCTCACGCATCTAAATTTAAGTGGCAACA 391
Qy 361 AAATTAAGAGCTCAGCACATAGAGCCCTGAAAGTTAGAAAACCTCGAGAGCTTAG 420
Db 392 AAATTAAGAGCTCAGCACATAGAGCCACTGAAAAGTTAGAAAACCTCAAGAGCTTAG 451
Qy 421 ACCTTTTCACTTGGAGGTAAACCAACCTGAACAACCTACTGAGAGAAAGTGTTCAGAGCTCC 480
Db 452 ACCTTTTCAATTCGAGGTAAACCAACCTGAACGACTACCGAGAAAATGTGTTCAGAGCTCC 511
Qy 481 TCCTGCAACTCACATATCTAACCGCTGTGACCCGGATGACAAGAGGCCCTTAACCTCGG 540
Db 512 TCCGCAACTCACATATCTGACGGCTATGACCGGGACGACAAGGAGGCCCTGACTCGG 571
Qy 541 ATGGTGGAGGCTTTGTGAGTGCCTGGATGACAGAGGAGGAGGTAGAGATGAGGAGGAGT 600
Db 572 ATGCTGAGGCTACGTGGAGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631
Qy 601 ATGATGAAGATGCTCAGGTAAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db 632 ATGATGAAGATGCTCAGGTAGTGAACACGAGGAGGAGGAGGATGAGGAGGAGGAGT 691
Qy 661 AAGAGGAGGAGCTGAGTGGAGACAGAGAGAGAGGATGAAGTATTAACAATGGAGAGG 720
Db 692 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGTATTAACAATGGAGAGG 751
Qy 721 TAGATGATGAGGAGATGAAGAGAGCTTGTGAAGAGAAAGGGTCAAGAGCGAAAAT 780
Db 752 TAGATGACGAGGAGATGAAGAGAGCTTGTGAAGAGAAAGGGTCAAGAGCGAAAAC 811
Qy 781 AAGAACTGAAGATGAGGAGAGACGATGCCTAAGTGAATATCTATTTCGAAAAT 840
Db 812 GAGAACTGAAGATGAGGAGAGATGATGACTAAGTGAATACCTATTTCGAAAAT 871
Qy 841 CCTTTTCTGATTTTACTGTTTATGCGGTACCCCTCTCCCGCCCACTTAATCCTGCC 900
Db 872 CCTATTGATTTGACTGTTTATACCATATCCCTCTCCCGCCCACTTAATCCTGCC 931
Qy 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 12

US-09-898-888A-14975
; Sequence 14975, Application US/0989888A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/898,888A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/340,623
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/205,070
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14975
; LENGTH: 2398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-888A-14975

Query Match 91.0%; Score 825.4; DB 33; Length 2398;
Best Local Similarity 94.4%; Pred. No. 7.6e-153;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1 GGGTTCGGGTTTATTGATTGATTCGGCTGCGCGGGAGCCTCTGCAGAGAGAGAGCGC 60
Db 32 GGGTTCGGGTTTATTGATTGATTCGGCTGCGCGGGAGCCTCTGCAGAGAGAGAGCGC 91

Qy 61 GAGAGATGGAGATGGGCACACGGAATTCATTTAGAGCTGGGACGGAGCCCTCTGTAGT 120
Db 92 GAGAGATGGAGATGGGCACACGGAATTCATTTAGAGCTGGGACGGAGCCCTCTGTAGT 151
Qy 121 TGAAGAACTTGTCCCTGGACACAGTCGGTCGATGAAGGCAAACTCGAAGGCTCACAG 180
Db 152 TGAAGAACTTGTCCCTGGACACAGTCGGTCGATGAAGGCAAACTCGAAGGCTCACAG 211
Qy 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTAACCTAGGCTCAGCTCAATCGCAA 240
Db 212 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTAACCTAGGCTCAGCTCAATCGCAA 271
Qy 241 ACTTACCAAGTTTAAACAACCTTAAGAAGCTTAAGCTAAGCAGTAAACAGAGCTCAGTGG 300
Db 272 ACTTACCAAGTTTAAACAACCTTAAGAAGCTTAAGCTAAGCAGTAAACAGAGCTCAGTGG 331
Qy 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAAGCTCATACTAATTTAAGTGGCAACA 360
Db 332 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAAGCTCATACTAATTTAAGTGGCAACA 391
Qy 361 AAATTAAGACCTTCAGCAACAATAGAGCCCTGAAAAGTTAGAAAACCTTCGAGAGCTTAG 420
Db 392 AAATTAAGACCTTCAGCAACAATAGAGCCACTGAAAAGTTAGAAAACCTTCAGAGCTTAG 451
Qy 421 ACCTTTTCACTTGGAGGTAAACCAACCTGAACAACCTACTGAGAGAGATGTTTCAAGCTCC 480
Db 452 ACCTTTTCAATTCGAGGTTAAACAACCTGACGAGCTTACCGAGAAAATGTGTTCAAGCTCC 511
Qy 481 TCCTGCAACTCACATATCTCAAGGCTGTGACCCGATGACAAAGGAGGCCCTTAAGTGG 540
Db 512 TCCCGCACTCACATATCTCGAGCGCTATGACCGGACGACAAGGAGGCCCTGACTCGG 571
Qy 541 ATGGTGGAGGCTTTTGTGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 572 ATGCTGAGGCTACGTGGAGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631
Qy 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660
Db 632 ATGATGAAGATGCTCAGGTAGTGAAGAGGAGGAGGAGGAGGATGAGGAGGAGGAGT 691
Qy 661 AAGAGGAGGAGTGTGAGTGGAGACGAGGAGGAGGAGGATGAAGGTTATACATGAGAGG 720
Db 692 AAGAGGAGGAGTGTGAGTGGAGAGGAGGAGGAGGATGAAGAGGTTATACATGAGAGG 751
Qy 721 TAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTCAAGAGCGAAAAT 780
Db 752 TAGATGACGAGGAGATGAAGAGAGCTTGTGAAGAGAAAGGGTCAAGAGCGAAAAC 811
Qy 781 AAGAACTGAAGATGAGGAGAGACGATGCCTAAGTGAATATCTATTTCGAAAAT 840
Db 812 GAGAACTGAAGATGAGGAGAGATGATGACTAAGTGAATACCTATTTCGAAAAT 871
Qy 841 CCTTTTGTGATTTTACTGTTTATAGCCCTACCCCTCTCCCGCCCACTTAATCCTGCC 900
Db 872 CCTATTGATTTGACTGTTTATACCATATCCCTCTCCCGCCCACTTAATCCTGCC 931
Qy 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 13

US-09-591-500-13
; Sequence 13, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodol, Shihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031/87.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06

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; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-09-591-500-13

Query Match      90.8%; Score 823.8; DB 22; Length 907;
Best Local Similarity 94.3%; Pred. No. 1.3e-152;
Matches 855; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATGATTGAATTCGGTGGCGGGAGGCTCTGCAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATGATTGAATTCGCGGGCGGGAGGCTCTGCAGAGAGAGAGCGC 60

QY 61 GAGAGATGAGATGGGACAGCGATTTCATTTAGAGCTGCGGAACGGGACGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGGACAGCGATTTCATTTAGAGCTGCGGACAGAGCGCCCTCTGATG 120

QY 121 TGAAGAAGCTTCTCTGGCAACACGTGCGTGAATGAAGGCAAACTCGAAGCCCTCAG 180
Db 121 TGAAGAAGCTTCTCTGGCAACACGTGCGTGAATGAAGGCAAACTCGAAGCCCTCAG 180

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGTAGGCTCACCCTCAATCGCAA 240
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGTAGGCTCACCCTCAATCGCAA 240

QY 241 ACTTACCAAGTTAAACAACTTGAAGCTTGAACCTAAGCAAGTAAACAGAGCTCAGTGG 300
Db 241 ACTTACCAAGTTAAACAACTTGAAGCTTGAACCTAAGCAAGTAAACAGAGCTCAGTGG 300

QY 301 GCGTGAAGTATTGGCAGAAAAGTGTCGGAAGCTCACGCATCTAAATTTAAGTGCAACA 360
Db 301 GCGTGAAGTATTGGCAGAAAAGTGTCGGAAGCTCACGCATCTAAATTTAAGTGCAACA 360

QY 361 AAATTTAAGACCTCAGCAACATAGAGCCACTGAAAGAGTTAGAAAACCTCAGAGCTTAG 420
Db 361 AAATTTAAGACCTCAGCAACATAGAGCCACTGAAAGAGTTAGAAAACCTCAGAGCTTAG 420

QY 421 ACCTTTTCACTTCGAGGTAACCAACTGAACAACTTACTGAGAGAGATGTTTCAAGCTCC 480
Db 421 ACCTTTTCACTTCGAGGTAACCAACTGAACAACTTACTGAGAGAGATGTTTCAAGCTCC 480

QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCCGATGACAAAGGAGGCCCTTAAGTTCG 540
Db 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCCGATGACAAAGGAGGCCCTTAAGTTCG 540

QY 541 ATGCTGAGGCTTGTGGAGTGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600
Db 541 ATGCTGAGGCTTGTGGAGTGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600

QY 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGAGT 660

QY 661 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGAGGTTTATACGATGGAGAGG 720
Db 661 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGAGGTTTATACGATGGAGAGG 720

QY 721 TAGATGATGAGGAGATGGAAGAGAGCTTGGTGAAGAAGAAAGGGCTCAGAAGCGAAAAAT 780
Db 721 TAGATGATGAGGAGATGGAAGAGAGCTTGGTGAAGAAGAAAGGGCTCAGAAGCGAAAAAT 780

QY 781 AAGAAACTGAAGATGAGGAGAGAGACGATGCGCTTAAGTGGAAATATCTATTTTGAAGAAAT 840
Db 781 AAGAAACTGAAGATGAGGAGAGAGACGATGCGCTTAAGTGGAAATATCTATTTTGAAGAAAT 840
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Db 781 GAGAACTGAAGATGAGGAGAGAGATGATGACTAAGTGAATAAACCTATTTTGAAGAAAT 840
QY 841 CCTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCGCCACACTCTAATCTCTGCC 900
Db 841 CCTATTGTGATTTGACTGTTTATACCCATATCCCTCTCCCGCCCTCTAATCTCTGCC 900
QY 901 CCCTGAA 907
Db 901 CCCTGAA 907

RESULT 14
US-09-591-500-25
; Sequence 25, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-591-500-25
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Query Match      90.7%; Score 822.2; DB 22; Length 907;
Best Local Similarity 94.2%; Pred. No. 2.8e-152;
Matches 854; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
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QY 1 GGGTTCGGGGTTTATGATTGAATTCGGTGGCGGGAGGCTCTGCAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATGATTGAATTCGCGGGCGGGAGGCTCTGCAGAGAGAGAGCGC 60

QY 61 GAGAGATGAGATGGGACAGCGATTTCATTTAGAGCTCGGGAACGGGACGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGGACAGCGATTTCATTTAGAGCTCGGGAACGGGACGCCCTCTGATG 120

QY 121 TGAAGAAGCTTGTCTCTGGCAACACGTGCGTGAATGAAGCAAACTCGAAGCCCTCAG 180
Db 121 TGAAGAAGCTTGTCTCTGGCAACACGTGCGTGAATGAAGCAAACTCGAAGCCCTCAG 180

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGTAGGCTCACCCTCAATCGCAA 240
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGTAGGCTCACCCTCAATCGCAA 240

QY 241 ACTTACCAAGTTAAACAACTTGAAGAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGG 300
Db 241 ACTTACCAAGTTAAACAACTTGAAGAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGG 300

QY 301 GCGTGAAGTATTGGCAGAAAAGTGTCGGAAGCTTGAACCTAAGGAGGAGGCCCTTAAGTG 360
Db 301 GCGTGAAGTATTGGCAGAAAAGTGTCGGAAGCTTGAACCTAAGGAGGAGGCCCTTAAGTG 360

QY 361 AAATTTAAGACCTCAGCAACATAGAGCCACTGAAAGAGTTAGAAAACCTCAGAGCTTAG 420
Db 361 AAATTTAAGACCTCAGCAACATAGAGCCACTGAAAGAGTTAGAAAACCTCAGAGCTTAG 420

QY 421 ACCTTTTCACTTCGAGGTAACCAACTGAACAACTTACTGAGAGAGATGTTTCAAGCTCC 480
Db 421 ACCTTTTCACTTCGAGGTAACCAACTGAACAACTTACTGAGAGAGATGTTTCAAGCTCC 480

QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCCGATGACAAAGGAGGCCCTTAAGTTCG 540
Db 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCCGATGACAAAGGAGGCCCTTAAGTTCG 540
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Db	481	TCCGCAACTCACATATCTCGACGCTATGACCGGGACGACAGAGGCCCTGACTCGG	540
Qy	541	ATGCTGAGGGCTTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGAGT	600
Db	541	ATGCTGAGGGCTACGTGGAGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	600
Qy	601	ATGATGAAGATGCTCAGTGAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT	660
Db	601	ATGATGAAGATGCTCAGTGAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT	660
Qy	661	AAGAGGAGGAGTGAAGTGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	720
Db	661	AAGAGGAGGAGTGAAGTGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	720
Qy	721	TAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGT	780
Db	721	TAGATGAGGAGGAGATGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGT	780
Qy	781	AAGAACTGAAGATGAGGAGGAGACGACCTGCTAAGTGGAGTAACTATCTATTTGAAAAAT	840
Db	781	GAGAACTGAAGATGAGGAGGAGACGACCTGCTAAGTGGAGTAACTATCTATTTGAAAAAT	840
Qy	841	CCTTTGTGATTTACTGTTTTAGCGGTACCCCTCTCCCGCCCACTCTAATCTCTGCC	900
Db	841	CCTATTGTGATTTACTGTTTTACCCTATATCCCTCTCCCGCCCACTCTAATCTCTGCC	900
Qy	901	CCCTGAA 907	
Db	901	CCCTGAA 907	

RESULT 15
US-09-591-500-28
; Sequence 28, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 28
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (65)..(812)
; OTHER INFORMATION:
US-09-591-500-28

Query Match 90.7%; Score 822.2; DB 22; Length 907;
Best Local Similarity 94.2%; Pred. No. 2.8e-152;
Matches 854; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy	1	GGTTCGGGTTTATTGATTGATTCGGCTGGCGGGGAGCCCTCTCCAGAGAGAGAGCGC	60
Db	1	GGTTCGGGTTTATTGATTGATTCGGCTGGCGGGGAGCCCTCTCCAGAGAGAGAGCGC	60
Qy	61	GAGAGATGAGATGGGACGAGGATTCATTAGAGCTCGGAAACGGAGCGCCCTCTGATG	120
Db	61	GAGAGATGAGATGGGACGAGGATTCATTAGAGCTCGGAAACGGAGCGCCCTCTGATG	120
Qy	121	TGAAGAAGTTGCTGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGGCTCACAG	180

Db	121	TGAAGAAGTTGCTGGTCAACAGTCGGTCGAATGAAGGCAAACTCGAAGGCTCACAG	180
Qy	181	ATGAATTTGAAGAACTGGAAATCTTAAAGTACAACTAACCTAGGCCCTACCTCAATCGCAA	240
Db	181	ATGAATTTGAAGAACTGGAAATCTTAAAGTACAACTAACCTAGGCCCTACCTCAATCGCAA	240
Qy	241	ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAAGCACTAAGCAGTAAACAGAGCTCAGTGG	300
Db	241	ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAAGCACTAAGCAGTAAACAGAGCTCAGTGG	300
Qy	301	GCTAGAACTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAAGTGGCAACA	360
Db	301	GCTAGAACTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAAGTGGCAACA	360
Qy	361	AAATTAAGACCTTCAGCACAATAGAGCCCTGAAAAGTTAGAAAACCTTCGAGAGCTAG	420
Db	361	AAATTAAGACCTTCAGCACAATAGAGCCCTGAAAAGTTAGAAAACCTTCAGAGCTTAG	420
Qy	421	ACCTTTTCACTTGGCAGGTAAACCACTGAACTACTGAGAGAGAGTGTTCAGAGCTCC	480
Db	421	ACCTTTTCACTTGGCAGGTAAACCACTGAACTACTGAGAGAGAGTGTTCAGAGCTCC	480
Qy	481	TCCTGCAACTCACATATCTCAACGGCTGTGACCGGATGACAAAGGAGGAGGAGGAGGAGT	540
Db	481	TCCTGCAACTCACATATCTCAACGGCTGTGACCGGATGACAAAGGAGGAGGAGGAGGAGT	540
Qy	541	ATGCTGAGGCTTGTGGAGTGCCTGGATGACAAAGGAGGAGGAGGAGGAGGAGGAGT	600
Db	541	ATGCTGAGGCTTGTGGAGTGCCTGGATGACAAAGGAGGAGGAGGAGGAGGAGGAGT	600
Qy	601	ATCATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT	660
Db	601	ATCATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT	660
Qy	661	AAGAGGAGGAGTGTGAGTGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT	720
Db	661	AAGAGGAGGAGTGTGAGTGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT	720
Qy	721	TAGATGATGAGGAGATGAAGAAGCTTGGTGAAGAAGAAAGGGGTGAGAGCGGAAAT	780
Db	721	TAGATGATGAGGAGATGAAGAAGCTTGGTGAAGAAGAAAGGGGTGAGAGCGGAAAT	780
Qy	781	AAGAACTGAAGATGAGGAGGAGAGGATGCTTAAGTGAATTAATCTATTTGAAAAAT	840
Db	781	AAGAACTGAAGATGAGGAGGAGAGGATGCTTAAGTGAATTAATCTATTTGAAAAAT	840
Qy	841	CCTTTTGTGATTTACTGTTTTAGCCGCTACCCCTCTCCCGCCCACTCTAATCTCTGCC	900
Db	841	CCTATTGTGATTTACTGTTTTACCCTATATCCCTCTCCCGCCCACTCTAATCTCTGCC	900
Qy	901	CCCTGAA 907	
Db	901	CCCTGAA 907	

Search completed: December 9, 2002, 00:32:10
Job time : 2187.68 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:58:38 ; Search time 56,5612 Seconds
(without alignments)
11105.648 Million cell updates/sec

Title: US-09-591-500-4

Perfect score: 907

Sequence: 1 ggggttcgggggtttattgatt.....ctctaactcgtcccccgtgaa 907

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 361435 seqs, 346278564 residues

Total number of hits satisfying chosen parameters: 722870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New.*
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6: /cgn2.6/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /cgn2.6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	907	100.0	907	6	US-10-273-334-4
2	884.6	97.5	907	6	US-10-273-334-4
3	857.8	94.6	905	6	US-10-273-334-19
4	857.8	94.6	905	6	US-10-273-334-19
5	856.2	94.4	905	6	US-10-273-334-26
6	833.4	91.9	907	6	US-10-273-334-9
7	827.8	91.3	906	6	US-10-273-334-33
8	823.8	90.8	907	6	US-10-273-334-33
9	822.2	90.7	907	6	US-10-273-334-13
10	822.2	90.7	907	6	US-10-273-334-25
11	817.8	90.2	905	6	US-10-273-334-28
12	812.8	88.6	908	6	US-10-273-334-32
13	801.8	88.4	905	6	US-10-273-334-11
14	782.2	86.2	907	6	US-10-273-334-6
15	751	82.8	895	6	US-10-273-334-23
16	738.2	81.4	895	6	US-10-273-334-21
17	736.6	81.2	895	6	US-10-273-334-15
18	716	78.9	889	6	US-10-273-334-3
19	716	78.9	716	6	US-10-273-334-1
20	375.8	41.4	1937	5	US-09-724-676-18913
21	375.8	41.4	1937	5	US-09-724-676-18913
22	129.4	14.3	147	5	US-09-513-999C-24429
23	109.2	12.0	3489	6	US-10-194-046-1
24	105.2	11.6	616	6	US-10-266-131-2731
25	101	11.1	659158	5	US-09-771-208A-20
26	100.4	11.1	648	6	US-10-152-319A-2106

ALIGNMENTS

RESULT 1

US-10-273-334-4

; Sequence 4, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kochevar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shrinharl S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 03187.0076

; CURRENT APPLICATION NUMBER: US/10/273,334

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 907

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-273-334-4

Query Match 100.0%; Score 907; DB 6; Length 907;

Best Local Similarity 100.0%; Pred. No. 3e-189;

Matches 907; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy	1	GGGTTCGGGGTTCGCTGAGTTCGCTGGCGGGAGCGCTCTGCAGAGAGAGCGC	60
Db	1	GGGTTCGGGGTTCGCTGAGTTCGCTGGCGGGAGCGCTCTGCAGAGAGAGCGC	60
Qy	61	GAGAGATGGAGATGGCGAGCGGATTCATTAGAGCTCGGAGCGGCGCTCTGATG	120
Db	61	GAGAGATGGAGATGGCGAGCGGATTCATTAGAGCTCGGAGCGGCGCTCTGATG	120
Qy	121	TGAAGAACTGTCTCGACACAGTCGGTCGATGAAGCAAACTCGAGGCTCACAG	180
Db	121	TGAAGAACTGTCTCGACACAGTCGGTCGATGAAGCAAACTCGAGGCTCACAG	180
Qy	181	ATGAATTTGAAGAACTGGAATTCCTTAAGTCAATCAACGTAGGCTCACATCGCA	240
Db	181	ATGAATTTGAAGAACTGGAATTCCTTAAGTCAATCAACGTAGGCTCACATCGCA	240
Qy	241	ACTTACCAGAGTTAAACAACTTAAGAGCTTAAGCAAGCTTAAGCAAGCTTAAG	300
Db	241	ACTTACCAGAGTTAAACAACTTAAGAGCTTAAGCAAGCTTAAGCAAGCTTAAG	300

US-10-273-334-19

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; Sequence 19, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(453)
; OTHER INFORMATION:
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US-10-273-334-19

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Query Match          94.6%; Score 857.8; DB 6; Length 905;
Best Local Similarity 97.4%; Pred. No. 1.7e-178;
Matches 883; Conservative 0; Mismatches 22; Indels 2; Gaps 1;

QY 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGGAGCCCTCTGAGAGAGAGCGC 60
DB 1 GGGTTCGGGGTTTATTGTTGAATTCGCTGGCTCAGGAGCCCTCTGC--AGAGAAAGCGT 58

QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTTAGAGCTGCGGAACGGGACGCCCTCTGATG 120
DB 59 GAGAGATGGAGATGGGCAATGATTCATTTAGAGCTGCGGAACGGGACGCCCTCCGATG 118

QY 121 TGAAGAACTTGTCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGGCCCTACAG 180
DB 119 TGAAGAACTTTCTTGACACAGTCAGTCAAAATGAAGGCAAAATGGAAGGCCCTACAG 178

QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACCTACATCTAAATTTAAGTGGCA 240
DB 179 ATGAATTTGAAGAACTGGAATTTATTAATACAATCAACATAGAGCCCTACCTCAATTGCAA 238

QY 241 ACTTACCAAAAGTTAAACAACTTAAGAAGCTTGAACCTAAGCAGTAACAGAGCCCTAGTGG 300
DB 239 ACTTGCCAAAGTTAAACAACTTAAGAGCTTGAAGCTGAACTAAGCAGTAACAGAGCCCTAGTGG 298

QY 301 GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
DB 299 GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 358

QY 361 AAATTAAAGACCTCAGCACAATAGAGCCCTGAAAAGTTAGAAACCTCGAGAGCTTAG 420
DB 359 AAATTAAAGACCTCAGCACAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 418

QY 421 ACCTTTTCACTTCGGAGGTAAACCAACTGAACAACTACTGAGAGAAAGATGTTCAAGCTCC 480
DB 419 ACCTTTTCACTTCGGAGGTAAACCAACTGAAACAACTACTGAGAAAAGATGTTCAAGCTCC 478

QY 481 TCCTGCAACTCAGATATCTCAACGGTGTGACCCGGATGACAGAGAGGCCCTTAAGTCCG 540
DB 479 TCCTGCAACTCAGATATCTCAACGGTGTGACCCGGATGACAGAGAGGCCCTTAAGTCCG 538

QY 541 ATGGTGAGGCTTTGTGGAGTCTGATGACAAAGAGAGGATGAGGATGAGGAGGAGT 600
DB 539 ATGGTGAGGCTTTGTGGAGTCTGATGACAAAGAGAGGAGGATGAGGATGAGGAGGAGT 598
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QY 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGACGAGGATGAGGAGGAGGAACTGTG 660
DB 599 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGACGAGGATGAGGAGGAGGAACTGTG 658
QY 661 AAGAGGAGGACGTGAGTGGAGAGGAGGAGGAGGAGGATGAAGGTTATACAAATGGAGAGG 720
DB 659 AAGAGGAGGACGTGAGTGGAGAGGAGGAGGAGGAGGATGAAGGTTATACAAATGGAGAGG 718
QY 721 TAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAAAGGGGTCAAGAGCGGAAAT 780
DB 719 TAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAAAGGGGTCAAGAGCGGAAAT 778
QY 781 AAGAACTGAAGATGAGGAGAGAGAGAGCGATGCCTTAAGTGAATAATCTATTTGAAAAATT 840
DB 779 AAGAACTGAAGATGAGGAGAGAGAGAGCGATGCCTTAAGTGAATAATCTATTTGAAAAATT 838
QY 841 CCTTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCGGATATCCCTCTCCCGGATAT 900
DB 839 CCTTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCGGATATCCCTCTCCCGGATAT 898
QY 901 CCTGTAA 907
DB 899 CCTGTAA 905
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RESULT 4

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US-10-273-334-26
; Sequence 26, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(453)
; OTHER INFORMATION:
US-10-273-334-26
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Query Match          94.6%; Score 857.8; DB 6; Length 905;
Best Local Similarity 97.4%; Pred. No. 1.7e-178;
Matches 883; Conservative 0; Mismatches 22; Indels 2; Gaps 1;
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QY 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGGAGCCCTCTGAGAGAGAGAGCGC 60
DB 1 GGGTTCGGGGTTTATTGTTGAATTCGCTGGCTCAGGAGCCCTCTGC--AGAGAAAGCGT 58

QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTTAGAGCTGCGGAACGGGACGCCCTCTGATG 120
DB 59 GAGAGATGGAGATGGGCAATGATTCATTTAGAGCTGCGGAACGGGACGCCCTCCGATG 118

QY 121 TGAAGAACTTGTCTTGACACAGTCGGTCAATGAAGGCAAACTCGAAGGCCCTACAG 180
DB 119 TGAAGAACTTTCTTGACACAGTCAGTCAAAATGAAGGCAAAATGGAAGGCCCTACAG 178

QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACCTACATCTAAATTTAAGTGGCA 240
DB 179 ATGAATTTGAAGAACTGGAATTTATTAATACAATCAACATAGAGCCCTACCTCAATTGCAA 238
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Db 179 ATGAATTTGAAGAACTGGAATTTAAATACAATCAATAGGCTCACCTCAATTCGAA 238
Qy 241 ACTTACCAAGTTAAACAACTTTAGAGCTTGAAGCTTAAGCAGTAACAGAGCCCTCAGTGG 300
Db 239 ACTTCCCAAGTTAAACAACTTTAGAGCTTGAAGCTTAAGCAGTAACAGAGCCCTCAGTGG 298
Qy 301 GCTAGAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 299 GCCTAGAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 358
Qy 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAGGTTAGAAAACCTCAGAGAGCTTAG 420
Db 359 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAGGTTAGAAAACCTCAGAGAGCTTAG 418
Qy 421 ACCTTTTACCTTGCAGAGTAAACCACTGAAACACTAGAGAGAGAGTGTCAAGCTCC 480
Db 419 ACCTTTTACCTTGCAGAGTAAACCACTGAAACACTAGAGAGAGAGTGTCAAGCTCC 478
Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCGCCCTAACTCGG 540
Db 479 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCGCCCTAACTCGG 538
Qy 541 ATGGTAGAGGCTTTGTGAGTGCCTGGATGACAGAGGAGGAGTGAAGGAGTGAAGGAGT 600
Db 539 ATGGTAGAGGCTTTGTGAGTGCCTGGATGACAGAGGAGGAGTGAAGGAGTGAAGGAGT 598
Qy 601 ATGATGAAGTCTCAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
Db 599 ATGATGAAGTCTCAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 658
Qy 721 TAGATGATGAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780
Db 719 TAGATGATGAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 778
Qy 781 AGAAACTCAAGTGAAGGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
Db 779 AGAAACTCAAGTGAAGGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 838
Qy 841 CCTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCTCCCTCCCTCCCTCCCTCC 900
Db 839 CCTTTGTGATTTTACTGTTTGTAGCCGTATCCCTCTCCCTCCCTCCCTCCCTCCCTCC 898
Qy 901 CCTGAA 907
Db 899 CCTGAA 905

RESULT 5
US-10-273-334-7
; Sequence 7, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 905

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(453)
; OTHER INFORMATION:
US-10-273-334-7
Query Match 94.4%; Score 856.2; DB 6; Length 905;
Best Local Similarity 97.2%; Pred. No. 3.7e-178;
Matches 882; Conservative 0; Mismatches 23; Indels 2; Gaps 1;
Qy 1 GGTTCCGGGTTTATTGATTAATTCGGCTGGCGCGGGAGCCCTCTCCAGAGAGAGAGCGC 60
Db 1 GGTTCCGGGTTTATTGATTAATTCGGCTGGCGCGGGAGCCCTCTCCAGAGAGAGAGCGC 58
Qy 61 GAGAGATGAGATGGGACAGAGATTCATTAGAGCTGGGAAACGGAGCGCCCTCTGATG 120
Db 59 GAGAGATGAGATGGGACAAATGGATTCATTAGAGCTGGGAAACGGAGCGCCCTCCGATG 118
Qy 121 TGAAGAACTTGTCTCGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGGCTCACAG 180
Db 119 TGAAGAACTTGTCTCGGACACAGTCAGTCAATGAAGGCAAAATTTGAAGGCTCACAG 178
Qy 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACGTAGGCGCTCACCTCAATCGCA 240
Db 179 ATGAATTTGAAGAACTGGAATTTAAATACAATCAACATAGGCGCTCACCTCAATTCGCA 238
Qy 241 ACITACCAAGTTTAAACAACTTAAAGAGCTTGAAGCTTAAGCAGTAAACAGAGCTCAGTGG 300
Db 239 ACITGCGCAAGTTTAAACAACTTAAAGAGCTTGAAGAGCTTGAAGCTTAAGCAGTAAACAG 298
Qy 301 GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 299 GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 358
Qy 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAGGTTAGAAAACCTCGAGAGCTTAG 420
Db 359 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAGGTTAGAAAACCTCGAGAGCTTAG 418
Qy 421 ACCTTTTCACCTTGGAGGTAAACCACTGAAACCTACTGAGAGAGATGTTCAAGCTCC 480
Db 419 ACCTTTTCACCTTGGAGGTAAACCACTGAAACCTACTGAGAGAGATGTTCAAGCTCC 478
Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAGAGGAGGCGCCCTAACTCGG 540
Db 479 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAGAGGAGGCGCCCTAACTCGG 538
Qy 541 ATGGTAGAGGCTTTGTGAGTGCCTGATGACAGAGGAGGAGTGAAGGAGTGAAGGAGT 600
Db 539 ATGGTAGAGGCTTTGTGAGTGCCTGATGACAGAGGAGGAGTGAAGGAGTGAAGGAGT 598
Qy 601 ATGATGAAGTCTCAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
Db 599 ATGATGAAGTCTCAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 658
Qy 661 AAGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 720
Db 659 AAGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 718
Qy 721 TAGATGATGAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 780
Db 719 TAGATGATGAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 778
Qy 781 AAGAACTGAAGTGAAGGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
Db 779 AAGAACTGAAGTGAAGGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 838
Qy 841 CCTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCTCCCTCCCTCCCTCCCTCC 900
Db 839 CCTTTGTGATTTTACTGTTTGTAGCCGTATCCCTCTCCCTCCCTCCCTCCCTCCCTCC 898
Qy 901 CCTGAA 907

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Db 899 CCCTGAA 905
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RESULT 6
US-10-273-334-9
; Sequence 9, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT FILING DATE: 2002-10-18
; PRIOR FILING DATE: 2002-10-18
; PRIOR FILING DATE: 2000-12-06
; PRIOR FILING DATE: 2000-12-06
; PRIOR FILING DATE: 1998-12-11
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-9

Query Match 91.3%; Score 833.4; DB 6; Length 907;
Best Local Similarity 94.9%; Pred. No. 3.5e-173;
Matches 861; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTATTGATTGAATTCGGCTGGCGCGGGAGCCCTCTCAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTATTGATTGAATTCGGCGCGGGAGCCCTCTCAGAGAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGCGAGAGCGGATTCATTAGAGCTGCGGAACGGGAGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCGAGAGCGGATTCATTAGAGCTGCGGAACGGGAGCCCTCTGATG 120
QY 121 TGAAGAACTTCCTCGGACAAAGTCGGTCGAATGAAGGCAAACTCGAAGGCGCTCACAG 180
Db 121 TGAAGAACTTCCTCGGACAAAGTCGGTCGAATGAAGGCAAACTCGAAGGCGCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCA 240
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCA 240
QY 241 ACTTACAAAGTTAAACAACTTAAAGCTTGAAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG 300
Db 241 ACTTGCACAAAGTTAAACAACTTAAAGCTTGAAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG 300
QY 301 GCTTAGAAGTATTGGCAGAAAGCTGCCAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 301 GCTTAGAAGTATTGGCAGAAAGCTGCCAACCTCATACATCTAAATTTAAGTGGCAACA 360
QY 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACTTCGAGAGCTTAG 420
Db 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACTTCAGAGCTTAG 420
QY 421 ACCTTTTCACTTCGGAGGTAAACCAACTGAACACTTACTGAGAGAGATGTTTCAAGCTCC 480
Db 421 ACCTTTTCAATTCGGAGGTAAACCAACTGAACACTTACCAGAGAAATGTTTCAAGCTCC 480
QY 481 TCCTGGAACTCATATCTCAACGGCTGTGACCCGGATGACAAAGAGAGGCCCTTAAGTGG 540
Db 481 TCCCGAACTCATATCTCGAGGGCTATGACGGGACGACAAAGAGAGGCCCTTAAGTGG 540
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QY 541 ATGGTGAGGGCTTTGTGGAGTGCCCTGGATGACAAAGAGAGGAGGATGAGGAGGAGT 600
Db 541 ATGGTGAGGGCTACGTGGAGGGCTTGATGATCAGGAGGAGGATGAGGAGGAGT 600
QY 601 ATGATGAAGATGCTCAGGTAATGTAAGATGAGGAGGAGGAGGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGGTAAGTAAGATGAGGAGGAGGAGGAGGAGGAGGAGT 660
QY 661 AAGAGGAGGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 661 AAGAGGAGGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 721 TAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAGGAGGAGGAGGAGGAGGAGT 780
Db 721 TAGATGACGAGGAAGATGAAGAGAGCTTGGTGAAGAGGAGGAGGAGGAGGAGGAGT 780
QY 781 AAGAAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Db 781 GAGAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
QY 841 CCTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCTCCCTCTCTAATCCTGCC 900
Db 841 CCTATTGTGATTTGACTGTTTACCCTATCCCTCTCCCTCCCTCTCTAATCCTGCC 900
QY 901 CCCTGAA 907
Db 901 CCCTGAA 907

RESULT 7
US-10-273-334-33
; Sequence 33, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273.334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591.500
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-33

Query Match 91.3%; Score 827.8; DB 6; Length 906;
Best Local Similarity 95.3%; Pred. No. 5.9e-172;
Matches 864; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 1 GGGTTCGGGGTTATTGATTGAATTCGGCTGGCGGGAGGAGGAGGAGGAGGAGGAG 60
Db 1 GGGTTCGGGGTTATTGATTGAATTCGGCTGGCGGGAGGAGGAGGAGGAGGAGGAGGAG 60
QY 61 GAGAGATGGAGATGGCGAGAGCGGATTCATTAGAGCTGCGGAACGGGAGGAGGAGGAGGAG 120
Db 61 GAGAGATGGAGATGGCGAGAGCGGATTCATTAGAGCTGCGGAACGGGAGGAGGAGGAGGAG 120
QY 121 TGAAGAACTTCCTCGGACAAAGTCGGTCGAATGAAGGCAAACTCGAAGGCGCTCACAG 180
Db 121 TGAAGAACTTCCTCGGACAAAGTCGGTCGAATGAAGGCAAACTCGAAGGCGCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCA 240
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCA 240
QY 241 ACTTACAAAGTTAAACAACTTAAAGCTTGAAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG 300
Db 241 ACTTGCACAAAGTTAAACAACTTAAAGCTTGAAGCTTGAACCTAAGCAGTAACAGAGCCTCAGTGG 300
QY 301 GCTTAGAAGTATTGGCAGAAAGCTGCCAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 301 GCTTAGAAGTATTGGCAGAAAGCTGCCAACCTCATACATCTAAATTTAAGTGGCAACA 360
QY 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACTTCGAGAGCTTAG 420
Db 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACTTCAGAGCTTAG 420
QY 421 ACCTTTTCACTTCGGAGGTAAACCAACTGAACACTTACTGAGAGAGATGTTTCAAGCTCC 480
Db 421 ACCTTTTCAATTCGGAGGTAAACCAACTGAACACTTACCAGAGAAATGTTTCAAGCTCC 480
QY 481 TCCTGGAACTCATATCTCAACGGCTGTGACCCGGATGACAAAGAGAGGCCCTTAAGTGG 540
Db 481 TCCCGAACTCATATCTCGAGGGCTATGACGGGACGACAAAGAGAGGCCCTTAAGTGG 540
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121 TGAAGAACTTGTCTGCACACAGTCGGTGAATGAAGGCAAACTCGAAGGCCTCACAG 180
181 ATGAATTTGAGAACTGGAATTTCTTAAGTACAATCAAGTAGGCTCACCTCAATCCAA 240
181 ATGAATTTGAGAACTGGAATTTCTTAAGTACAATCAAGTAGGCTCACCTCAATCCAA 240
241 ACTTACCAAGTTAAACAACTTAAGAGCTTGAACAGTAAGCAGTAACAGAGCCTCAGTGG 300
241 ACTTACCAAGTTAAACAACTTTAGAGCTTGAACAGTAAGCAGTAAGCAGTAAGCAGTGG 300
301 GCCTAGAAGTTAGCGCAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
301 GCCTAGAAGTTAGCGCAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
361 AAATTAAGACCTCAGCACATAGAGCCCTGAAAGGTTAGAAAACCTCGAGAGCTTAG 420
361 AAATTAAGACCTCAGCACATAGAGCCCTGAAAGGTTAGAAAACCTCGAGAGCTTAG 420
421 ACCTTTTCACTTTCGAGGTAAACCACTGAAACCTACTGAGAGAAGATGTTCAAGCTCC 480
421 ACCTTTTCACTTTCGAGGTAAACCACTGAAACCTACTGAGAGAAGATGTTCAAGCTCC 480
481 TCCTGCAACTCATATCTCAACGGCTGTGACCCGGATGACAAGGAGGAGTGAAGCTCGG 540
481 TCCTGCAACTCATATCTCAACGGCTGTGACCCGGATGACAAGGAGGAGTGAAGCTCGG 540
541 ATGGTGAAGGCTTTGTGAGTCCCTGGATGACAGAGGAGGAGTGAAGCTCGGAGGAGT 600
541 ATGGTGAAGGCTTTGTGAGTCCCTGGATGACAGAGGAGGAGTGAAGCTCGGAGGAGT 600
601 ATGATGAAGATGCTCAGGTAAATGGAAGTGAAGGAGGAGGAGTGAAGCTCGGAGGAGT 660
601 ATGATGAAGATGCTCAGGTAAATGGAAGTGAAGGAGGAGGAGTGAAGCTCGGAGGAGT 660
721 TAGATGATGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAAAT 780
721 TAGATGATGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAAAT 780
781 AAGAACTGAAGATGAGGAGGAGGAGTGAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGT 840
781 AAGAACTGAAGATGAGGAGGAGGAGTGAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGT 840

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; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-13

Query Match          90.8%; Score 823.8; DB 6; Length 907;
Best Local Similarity 94.3%; Pred. No. 4.4e-171;
Matches 855; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GGGTTCCGGGTTTATTGATTGGAATTCGGCTGGCGGGGAGCCCTCTGCAGAGAGAGAGCCG 60
DB 1 GGGTTCCGGGTTTATTGATTGGAATTCGGCTGGCGGGGAGCCCTCTGCAGAGAGAGAGCCG 60
QY 61 GAGAGATGGAGATGGCGACAGCGGATTCTATTAGAGCTGCGGAACGGGAGCGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGCGACAGCGGATTCTATTAGAGCTGCGGAACGGGAGCGCCCTCTGATG 120
QY 121 TGAAGAAGCTTGTCTCTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCTCACAG 180
DB 121 TGAAGAAGCTTGTCTCTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCTCACAG 180
QY 181 ATGAATTTGAGAACTGGAATTTCTTAAGTACATCAACCTAGGCTCAGCTCAATCGCAA 240
DB 181 ATGAATTTGAGAACTGGAATTTCTTAAGTACATCAACCTAGGCTCAGCTCAATCGCAA 240
QY 241 ACTTACCAAGTTAAACAACTTTAAGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 300
DB 241 ACTTACCAAGTTAAACAACTTTAAGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 300
QY 301 GCCTAGAAGTATTGGCGAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
DB 301 GCCTAGAAGTATTGGCGAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
QY 361 AAATTAAGACCTCAGCACATAGAGCCCTGAAAGGTTAGAAAACCTCGAGAGCTTAG 420
DB 361 AAATTAAGACCTCAGCACATAGAGCCCTGAAAGGTTAGAAAACCTCGAGAGCTTAG 420
QY 421 ACCTTTTCACTTTCGAGGTAAACCAACCTGAAACCTACTGAGAGAAGATGTTCAAGCTCC 480
DB 421 ACCTTTTCACTTTCGAGGTAAACCAACCTGAAACCTACTGAGAGAAGATGTTCAAGCTCC 480
QY 481 TCCTGCAACTCATATCTCAACGGCTGTGACCCGGATGACAAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 TCCTGCAACTCATATCTCAACGGCTGTGACCCGGATGACAAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 ATGGTGAAGGCTTTGTGAGTCCCTGGATGACAGAGGAGGAGGAGTGAAGCTCGGAGGAGT 600
DB 541 ATGGTGAAGGCTTTGTGAGTCCCTGGATGACAGAGGAGGAGTGAAGCTCGGAGGAGT 600
QY 601 ATGATGAAGATGCTCAGGTAAATGGAAGTGAAGGAGGAGGAGTGAAGCTCGGAGGAGGAGGAGT 660
DB 601 ATGATGAAGATGCTCAGGTAAATGGAAGTGAAGGAGGAGGAGTGAAGCTCGGAGGAGGAGGAGT 660
QY 661 AAGAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 661 AAGAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 TAGATGATGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAAAT 780
DB 721 TAGATGATGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAAAT 780
QY 781 AAGAACTGAAGATGAGGAGGAGGAGTGAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 840
DB 781 AAGAACTGAAGATGAGGAGGAGGAGTGAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 840

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QY 841 CCTTTGTGATTTACTGTTTTAGCCGTACCCCTCTCCGCCCACTCTAATCCTGCC 900
Db 841 CCTATTGTGATTTGACTGTTTTTACCCATATCCCTCTCCGCCCCCTCTAATCCTGCC 900
QY 901 CCCTGAA 907
Db 901 CCCTGAA 907

RESULT 9
US-10-273-334-25
; Sequence 25, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrinari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-25

Query Match 90.7%; Score 822.2; DB 6; Length 907;
Best Local Similarity 94.2%; Pred. No. 9.9e-171;
Matches 854; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTTGGCTGGCGGGAGCCCTCTCGAGAGAGAGCCG 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGAGCCCTCTCGAGAGAGAGCCG 60
QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGAGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGAGCCCTCTGATG 120
QY 121 TGAAGAACTTGTCTCGGACACAGTCGGTGAATGAAGCGCAACTCGAGGCTCACAG 180
Db 121 TGAAGAACTTGTCTCGGACACAGTCGGTGAATGAAGCGCAACTCGAGGCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACGTAGGCCCTCACTCAATCGCA 240
Db 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACGTAGGCCCTCACTCAATCGCA 240
QY 241 ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAAGCTTAAGCTTAAGCTTAAGCTTAAG 300
Db 241 ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAAGCTTGAAGCTTAAGCTTAAGCTTAAG 300
QY 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAATTTAAGTGGCAACA 360
Db 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAATTTAAGTGGCAACA 360
QY 361 AAATTAAGACCTTCAGCACATAGAGCCCTGAAAAGTTAGAAAACCTTCGAGAGCTTAG 420
Db 361 AAATTAAGACCTTCAGCACATAGAGCCCTGAAAAGTTAGAAAACCTTCAGAGCTTAG 420
QY 421 ACCTTTTCACTTCGAGGTAAACCAACCTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
Db 421 ACCTTTTCACTTCGAGGTAAACCAACCTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
QY 481 TCTGCAACTTCATATCTCAACGGCTGTGACCGGATGACAGAGAGGCCCTTACTCGG 540
Db 481 TCTGCAACTTCATATCTCAACGGCTGTGACCGGATGACAGAGAGGCCCTTACTCGG 540
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Db 481 TCCGCAACTCACATATCTCGAGCGGCTATGACGGGACGACAAAGAGGCCCTGACTCGG 540
QY 541 ATGGTGAAGGCTTTGTGGAGTCCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 541 ATGGTGAAGGCTTTGTGGAGTCCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
QY 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
QY 661 AAGAGGAGGAGGAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 720
Db 661 AAGAGGAGGAGGAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 720
QY 721 TAGATGATGAGGAAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 780
Db 721 TAGATGATGAGGAAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 780
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Db 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
QY 841 CCTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCGCCCACTCTAATCCTGCC 900
Db 841 CCTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCGCCCACTCTAATCCTGCC 900
QY 901 CCCTGAA 907
Db 901 CCCTGAA 907

RESULT 10
US-10-273-334-28
; Sequence 28, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrinari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-28

Query Match 90.7%; Score 822.2; DB 6; Length 907;
Best Local Similarity 94.2%; Pred. No. 9.9e-171;
Matches 854; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTCGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTCGAGAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGAGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGAGCCCTCTGATG 120
QY 121 TGAAGAACTTGTCTCGGACACAGTCGGTGAATGAAGCGCAACTCGAGGCTCACAG 180
Db 121 TGAAGAACTTGTCTCGGACACAGTCGGTGAATGAAGCGCAACTCGAGGCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACGTAGGCCCTCACTCAATCGCA 240
Db 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACGTAGGCCCTCACTCAATCGCA 240
QY 241 ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAAGCTTAAGCTTAAGCTTAAGCTTAAG 300
Db 241 ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAAGCTTGAAGCTTAAGCTTAAGCTTAAG 300
QY 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAATTTAAGTGGCAACA 360
Db 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAATTTAAGTGGCAACA 360
QY 361 AAATTAAGACCTTCAGCACATAGAGCCCTGAAAAGTTAGAAAACCTTCGAGAGCTTAG 420
Db 361 AAATTAAGACCTTCAGCACATAGAGCCCTGAAAAGTTAGAAAACCTTCAGAGCTTAG 420
QY 421 ACCTTTTCACTTCGAGGTAAACCAACCTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
Db 421 ACCTTTTCACTTCGAGGTAAACCAACCTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
QY 481 TCTGCAACTTCATATCTCAACGGCTGTGACCGGATGACAGAGAGGCCCTTACTCGG 540
Db 481 TCTGCAACTTCATATCTCAACGGCTGTGACCGGATGACAGAGAGGCCCTTACTCGG 540
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QY 841 CTTTGTGATTTACTGTTTGTAGCGGTACCCCTCTCCCGCCCACTCTAATCCTGCC 900
Db 839 CCTATTGTAATTGACTGTTTGTAGCGGTATCCCTCTCCCGCCCACTCTAATCCTGCC 898
QY 901 CCCTGAA 907
Db 899 CCCTGAA 905
RESULT 12
US-10-273-334-32
; Sequence 32, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-32

Query Match 89.6%; Score 812.8; DB 6; Length 908;
Best Local Similarity 94.2%; Pred. No. 1.1e-168;
Matches 855; Conservative 0; Mismatches 52; Indels 1; Gaps 1;
QY 1 GGGTTCGGGTTTATTGATTGAATTCGGTGGCGGGAGCCCTCTCAGAGAGAGAGCGG 60
Db 1 GGGTTCGGGTTTATTGATTGAATTCGGTGGCGGGAGCCCTCTCAGAGAGAGAGCGG 60
QY 61 -GAGAGATGAGATGGCAGACGATTCATTTAGAGCTCGGAAAGGAGCGCCCTCTGAT 119
Db 61 GGAGAGATGAGATGGCAGACGATTCATTTAGAGCTCGGAAAGGAGCGCCCTCTGAT 120
QY 120 GTCAAGAACTTGTCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCACA 179
Db 121 GTCAAGAACTTGTCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCACA 180
QY 180 GATGAATTTGAAGAACTTGAATTTAAAGAGCTTGAAGAGCTTAAGCAGTAACAGAGCCTCAGTG 239
Db 181 GATGAATTTGAAGAACTTGAATTTAAAGAGCTTGAAGAGCTTAAGCAGTAACAGAGCCTCAGTG 240
QY 240 AACTTACCAAGTTAACAACAACTTAAGAAGCTTGAAGAGCTTGAAGAGCTTAAGCAGTAACAGAGCCTCAGTG 299
Db 241 AACTTACCAAGTTAACAACAACTTAAGAAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCCTCAGTG 300
QY 300 GGCTTGAAGTTATGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAAC 359
Db 301 GGCTTGAAGTTATGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAAC 360
QY 360 AAAATTTAAAGACTCAGCACATAGAGCCCTGAAAAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCCTCAGTG 419
Db 361 AAAATTTAAAGACTCAGCACATAGAGCCCTGAAAAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCCTCAGTG 420
QY 420 GACCTTTTCACTTGGAGGTAACCAACCTGAACAACTACTGAGAGAAAGATGTTCAAGCTC 479
Db 421 GACCTTTTCACTTGGAGGTAACCAACCTGAACAACTACTGAGAGAAAGATGTTCAAGCTC 480
QY 480 CTCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAGAGGAGGCGCCCTTAACCTCG 539

Db 481 CTCCTGCAACTCACATATCTGACGGCTATGACCGGGAGCAAGGAGGCGCCCTGACTCG 540
QY 540 GATGGTGAGGCTTTGTGGAGTCCCTGGATGACAAGGAGGAGGATGAGATGAGGAGGAG 599
Db 541 GATGCTGAGGCTTACGTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 600
QY 600 TATGATGAAGATGCTCAGGTATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAG 659
Db 601 TATGATGAAGATGCTCAGGTATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAG 660
QY 660 GAAGAGGAGGAGTGTGAGTGTGAGGAGGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGAG 719
Db 661 GAAGAGGAGGAGTGTGAGTGTGAGGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGAG 720
QY 720 GTAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 779
Db 721 GTAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 780 TAAGAACTTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 839
Db 781 CGAGAACTTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 840 TCCTTTTGTGATTTACTGTTTGTAGCCCTACCCCTCTCCCGCCCACTCTAATCCTGC 899
Db 841 TCCTTTTGTGATTTACTGTTTGTAGCCCTACCCCTCTCCCGCCCACTCTAATCCTGC 900
QY 900 CCCCTGAA 907
Db 901 CCCCTGAA 908
RESULT 13
US-10-273-334-11
; Sequence 11, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(810)
; OTHER INFORMATION:
US-10-273-334-11

Query Match 88.4%; Score 801.8; DB 6; Length 905;
Best Local Similarity 93.5%; Pred. No. 2.8e-166;
Matches 848; Conservative 0; Mismatches 57; Indels 2; Gaps 1;
QY 1 GGGTTCGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCTCTGAGAGAGAGAGCGG 60
Db 1 GGGTTCGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCTCTGAGAGAGAGAGCGG 58
QY 61 GAGAGATGAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
Db 59 GAGAGATGAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 118

Db 841 CCTATTGTGATTTGACTGTTTTTACCACATATCCCTCTCTCCCCCCCCTCTAATCTCTGCC 900
QY 901 CCCTGAA 907
|||||
Db 901 CCCTGAA 907
RESULT 15
US-10-273-334-23
; Sequence 23. Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-10-273-334-23

Query Match 82.8%; Score 751; DB 6; Length 895;
Best Local Similarity 91.0%; Pred. No. 3.5e-155;
Matches 825; Conservative 0; Mismatches 70; Indels 12; Gaps 2;
QY 1 GGGTTCCGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGCGC 60
Db 1 GGGTTCCGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGCGACAGGATTCATTAGAGCTGCGAACGGAGCGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCGACAGGATTCATTAGAGCTGCGAACGGAGCGCCCTCTGATG 120
QY 121 TGAAGAAGCTTGTCTGGACACAGTCGGTTCGAATGAAGGCCAACTCGAAGGCCCTCACAG 180
Db 121 TGAAGAAGCTTGTCTGGACACAGTCGGTTCGAATGAAGGCCAACTCGAAGGCCCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTAACCTAGCGCTCAATCGCAA 240
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTAACCTAGCGCTCAATCGCAA 240
QY 241 ACTTACCAAGTTAAACAACTTAAGAAGCTTGAAGTAACTAGCAGTAACTAGAGCTCAGTGG 300
Db 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAAGTAACTAGCAGTAACTAGAGCTCAGTGG 300
QY 301 GCGTAGAAGTATGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 301 GCGTAGAAGTATGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
QY 361 AAATTAAAGACCTCAGCAACATAGAGCCCTGAAAAGTTAGAAACCTCGAGAGCTTAG 420
Db 361 AAATTAAAGACCTCAGCAACATAGAGCCCTGAAAAGTTAGAAACCTCGAGAGCTTAG 420
QY 421 ACCTTTTCACTTGCAGAGTAAACCACTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
Db 421 ACCTTTTCACTTGCAGAGTAAACCACTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
QY 480 ACCTTTTCACTTGCAGAGTAAACCACTGAACAACTACTGAGAGAGATGTTCAAGCTTC 468
Db 480 ACCTTTTCACTTGCAGAGTAAACCACTGAACAACTACTGAGAGAGATGTTCAAGCTTC 468

QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGAGGCGCCCTAACTCGG 540
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 19:17:03 ; Search time 1647.82 Seconds
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	889	100.0	70449	9	AC105250	Homo sapi
	3	764.2	86.0	1136	9	BC007200	Homo sapi
	4	761	85.6	1052	6	AK009985	Sequence 1
	5	761	85.6	1052	6	I91514	Sequence 1
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	8	756.2	85.1	916	9	HSPHAPI	H.sapiens m
	9	720.2	81.0	925	9	AF025684	Homo sapi
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C	11	671	75.5	162482	9	AC022740	Homo sapi
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	16	602.4	67.8	1017	10	RATLANP	D32209 rat mRNA fo
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	23	512.8	57.7	771	9	BC000608	Homo sapi
	24	483.8	54.4	1656	9	AY007110	Homo sapi
	25	438.2	49.3	101819	2	AC129809	Rattus no
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	37	284.4	32.0	168182	2	AC068338	Homo sapi
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	39	272.8	30.7	1225	10	AB025581	Rattus no
	40	264.6	29.8	1397	10	BC003489	Mus muscu
	41	264.6	29.8	1408	10	BC003628	Mus muscu
	42	263.6	29.7	1127	10	AB025582	Mus muscu
	43	260.8	29.3	238142	2	AL611930	Mus muscu
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ALIGNMENTS

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DEFINITION	Homo sapiens candidate tumor suppressor pp32r1 (PP32R1) gene, complete cds.
ACCESSION	AF008216
VERSION	AF008216.1 GI:2738512
KEYWORDS	.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	Kadkol,S.S., Brody,J.R., Pevsner,J., Bai,J. and Pasternack,G.R. 1 (bases 1 to 5785)
AUTHORS	Modulation of oncogene potential by alternative gene use in human
TITLE	

```

prostate cancer
Nature Medicine (1999) In press
2 (bases 1 to 5785)
Kochevar,G.J., Brody,J.R. and Pasternack,G.R.
The Structure of a Gene Encoding pp32r1, a New Member of the pp32
Family
Unpublished
3 (bases 1 to 5785)
Kochevar,G.J., Brody,J.R. and Pasternack,G.R.
Direct Submission
Submitted (13-JUN-1997) Pathology, Johns Hopkins University School
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Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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prostate cancer
Nature Medicine (1999) In press
2 (bases 1 to 5785)
Kochevar,G.J., Brody,J.R. and Pasternack,G.R.
The Structure of a Gene Encoding pp32r1, a New Member of the pp32
Family
Unpublished
3 (bases 1 to 5785)
Kochevar,G.J., Brody,J.R. and Pasternack,G.R.
Direct Submission
Submitted (13-JUN-1997) Pathology, Johns Hopkins University School
of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA
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by GenBank Accession Number U73477, SSP29, encoded by
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BASE COUNT 1755 a 1087 c 1162 g 1781 t
ORIGIN

Query Match 100.0%; Score 889; DB 9; Length 5785;
Best Local Similarity 100.0%; Pred. No. 4.8e-149;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTTCGAGGTTTATTGATTGNAATTCGGCTGGCAGGAGGCTCTGCAGACAGAGAGCGC 60
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DEFINITION Homo sapiens BAC clone RP11-39C10 from 4, complete sequence.
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VERSION AC105250.3 GI:19310326
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 70449)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 70449)
AUTHORS Desai,A., Creason,K. and Kozlowicz,A.
TITLE The sequence of Homo sapiens BAC clone RP11-39C10
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 70449)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 70449)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Mar 9, 2002 this sequence version replaced gi:18376931.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc

Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0039c10
Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/qsc>

SOURCE INFORMATION:

The RPI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P. Y., Zhao, B., Frangen, E., Tateno, M., Catanesi, J. and de Jong, P. J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pletier de Jong and coworkers at <http://www.chori.org> VECTOR: pBACs3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-360H22, 2000 bp overlap; the clone sequenced to the right is RP11-808H17, 2000 bp overlap. Actual start of this clone is at base position 97207 of RP11-360H22; actual end is at base position 22714 of RP11-808H17.

The sequence of AC011026 has been incorporated into AC105250.

Contact: sapiens@wustl.wustl.edu

----- Summary Statistics

Center project name: H_NH0039C10

Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sequences once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanesi, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-360H22, 2000 bp overlap; the clone sequenced to the right is RP11-808H17, 2000 bp overlap. Actual start of this clone is at base position 97207 of RP11-360H22; actual end is at base position 22714 of RP11-808H17.

The sequence of AC011026 has been incorporated into AC105250.

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Best Local Similarity									93.0%; Pred. No. 9e-127;
Matches	823;	Conservative	0;	Mismatches	50;	Indels	12;	Gaps	2;
QY	1	GGGTCGAGGTTT	TATGATTGA	ATTCGGCTGGCAGAGAGCCCT	TGCAGACAGAGAGCGC	60			
Db	69	GGGTCGGGTTT	TATGATTGA	ATTCGCGCGCGCGGAGCCT	CTGCAGAGAGAGCGC	128			
QY	61	GAGAGATGGAGAT	GCGCAGACGGAT	TCAATTCAGAGCTGCGGAACAGCGCGCCCT	CTCATG	120			
Db	129	GAGAGATGGAGAT	GCGCAGACGGAT	TCAATTCAGAGCTGCGGAACAGCGCGCCCT	CTCATG	188			
QY	121	TGAAAGAACTT	TGCCCTGGCAACAGCT	CGGTGCAATGAAGCAAACTCGAAGCCCT	CACAG	180			
Db	189	TGAAAGAACTT	TGCTGGCAACAGCT	CGGTGCAATGAAGCAAACTCGAAGCCCT	CACAG	248			
QY	181	ATGAATTTGAAGAACT	TGGAATTCCTTAAGTAAAT	TCACAGGAGGCCCTCACCTCAATCTCAG	240				
Db	249	ATGAATTTGAAGAACT	TGGAATTCCTTAAGTAAAT	TCACAGGAGGCCCTCACCTCAATCTCAG	308				
QY	241	ACTTACCAAAAGT	TAA--	AACTTCGAGAAAGCTTGAAC	TAAAAAGAGCTTCAAGCTT	288			
Db	309	ACTTACCAAAAGT	TAA--	AACTTCGAGAAAGCTTGAAC	TAAAAAGAGCTTCAAGCTT	368			
QY	289	GCCTGGAAGT	TATGGCAGAAAAAGT	TGTCCAAACCTTCACGCTCAT	TATATTAAAGTGGCAACA	348			
Db	369	GCCTGGAAGT	TATGGCAGAAAAAGT	TGTCCGAACTTCACGCTCAT	TATATTAAAGTGGCAACA	428			
QY	349	AAATTAAGACCT	CACGACCAATAGAGCCACT	GTAAACAGTTAGAAAACCTCAAGAGCTTAG	408				
Db	429	AAATTAAGACCT	CACGACCAATAGAGCCACT	GTAAAAAAGTTAGAAAACCTCAAGAGCTTAG	488				
QY	409	ACCTTTTCAAT	TGCGAGGTAAACCAACCT	GTAAACGACTACGGAGAAAAGCTG	TCAAGCTTC	468			
Db	489	ACCTTTTCAAT	TGCGAGGTAAACCAACCT	GTAAACGACTACGGAGAAAAGT	TGTTCAAGCTTC	548			
QY	469	TCCTGCAACT	CACATATCTCGACAGCTG	TACTGGGACCAACAAGGAGGCCCTTACTCAG	528				
Db	549	TCCTGCAACT	CACATATCTCGAGGCT	TATGACGGGACGACAAAGGAGGCCCTGACTCGG	608				
QY	529	ATATTGAGGAC	CACTGGAGGGCT	CGATCACGAGGAGGAGGCTGACATCAGGAGGAGT	588				
Db	609	ATCTGAGGGCT	ACGTTGAGGGCT	CGATGATGAGGAGGAGTGAAGGATGAGGAGGAGT	668				
QY	589	ATGATGAAGAT	GTCTCAGGTAGTGAAGAT	GAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT	648				
Db	669	ATGATGAAGAT	GTCTCAGGTAGTGAAGAT	GAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT	728				
QY	649	AAGAGAGGAC	GTAGTTGGAGGGAC	GACGAGGATGAAGAAGTTATACGATGGAGAGG	708				
Db	729	AAGAGAGGAC	GTAGTTGGAGGGAC	GACGAGGATGAAGAAGTTATACGATGGAGAGG	788				
QY	709	TGATGCGGAGG	AGAGTGAAGAGCTT	CGTGAAGAAGAAAGGGGTCAAGCGGAAAT	768				
Db	789	TGATGCGGAGG	AGAGTGAAGAGCTT	CGTGAAGAAGAAAGGGGTCAAGCGGAAAT	848				
QY	769	GAGAACCT	TGAAGATGAGGGAGAGAT	GATGACTAAAGTAGAATTAACCTATTTTGAAGAAAT	828				
Db	849	GAGAACCT	TGAAGATGAGGGAGAGAT	GATGACTAAAGTAGAATTAACCTATTTTGAAGAAAT	908				
QY	829	CCATATTG	TGATTGACTGTTTTT	TACCCATATCCCTCCCCCTCC	873				
Db	909	CCATATTG	TGATTGACTGTTTTT	TACCCATATCCCTCCCCCTCC	953				

DEFINITION	Sequence 1 from patent US 5756676.			
ACCESSION	AR009985			
VERSION	AR009985.1 GI:3968790			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1052)			
TITLE	Pasternack,G.R.			
JOURNAL	Mammalian protein associated with uncontrolled cell division			
FEATURES	Patent: US 5756676-A 1 26-MAY-1998;			
	Location/Qualifiers			
source	1..1052			
BASE COUNT	/organism="unknown"			
ORIGIN	326 a 196 c 316 g 214 t			
	Query Match 85.6%; Score 761; DB 6; Length 1052;			
	Best Local Similarity 92.5%; Pred. No. 3.3e-126;			
	Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps			
Qy	1	GGGTTGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGAGCCCTTCGACAGACAGAGCGC 60		
Db	32	GGGTTGCGGGTTTATTGATTGAATTCGCGCGCGCGGGAGCCCTTCGACAGAGAGAGCGC 91		
Qy	61	GAGAGATGGAGATGGGCAGACGGATTATTTCAGAGCTGCGGAACAGAGGGCGCCCTCTGATG 120		
Db	92	GAGAGATGGAGATGGGCAGACGGATTATTTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 151		
Qy	121	TGAAGAAGACTTGCCTCGACCAACAGTCGGTCGATGAAGCGCAACCTCGAGCGCCTCACAG 180		
Db	152	TGAAGAAGACTTGTCTCGACACAGTCGGTCGATGAAGCGCAACCTCGAGCGCCTCACAG 211		
Qy	181	ATGAATTTGAAGAACTCGGAATCTTTAAGTAAAACTAACCGAGAGCCCTCACTCAATCTCAG 240		
Db	212	ATGAATTTGAAGAACTCGGAATCTTTAAGTAACTAACCTCAACCTAGAGCCCTCACTCAATCGCAA 271		
Qy	241	ACTTACCAGAGTTA- --AAGTTGAGAAAGCTTGAACTA- -----AGAGTCTCAGGGG 288		
Db	272	ACTTACCAGAGTTTAAACAACACTTAAGAAGCTTGAACCTAAGCGGATAACAGAGTCTCAGGGG 331		
Qy	289	GCCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348		
Db	332	GCCTPAGAAGTATTGGCAGAAAAAGTGTCCGAACCTCAGCATCTAATTTAAGTGGCAACA 391		
Qy	349	AAATTAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGAAAAACCTCAAGAGGCTTAG 408		
Db	392	AAATTAAGACCTCAGCACAAATAGAGCCACTGAAGGCACTGAAAAAGTTAGAAAAACCTCAAGAGGCTTAG 451		
Qy	409	ACCTTTTCAATTGGAGGTTAACCAACTGAACCACTACGGAGAGAAACGTGTTCACAGTTC 468		
Db	452	ACCTTTTCAATTGGAGGTTAACCAACTGAACCACTACCGAGAGAAATGTGTCAAGTCC 511		
Qy	469	TCCTGCAACTCACATATCTCGACAGCTGTGTACTGGGACCACAGAGAGGCCCTTACTTCAG 528		
Db	512	TCGCGCAACTCACATATCTCGAGGCTATGACCGGGACGACAGAGGCCCTGACTTCGG 571		
Qy	529	ATATTGAGGACCAGTGGAGGGGCTGGATGACGAGAGGAGGGTGATGAGGAGGAGT 588		
Db	572	ATGCTGAGGGCTACGTGGAGGGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631		
Qy	589	ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGAGGTTG 648		
Db	632	ATGATGAAGATGCTCAGGTAGTGGAGACGAGGAGGACGAGGATGAGGAGGAGAGGTTG 691		
Qy	649	AAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTTATAACGATGGAGGG 708		
Db	692	AAGAGGAGGACGTGAGTGGAGAGGAGGAGGAGGATGAAGAAGGTTTATAACGATGGAGGG 751		
Qy	709	TAGATGCGGAGGAGATGAGAGAGACCTTGGTCAAGAGAAAGGGGTTCAGACCGCAAAAT 768		
Db	752	TAGATACGAGGAGAGATGAAGAAGACCTTGGTGAAGAAGAAAGGGGTTCAGACCGCAAAAC 811		

QY 769 GAGAACCTGAAGATGAGGGAGAAGATGATGACTAAGTAGAATAACCTATTATTTGAAAAATT 828
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LOCUS I91514 1052 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5726018.
ACCESSION I91514
VERSION I91514.1 GI:3935984
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Nucleic acid based assays to detect a novel mammalian protein
associated with uncontrolled cell division
JOURNAL Patent: US 5726018-A 1 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..1052
/organism="unknown"
BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN

Query Match 85.6%; Score 761; DB 6; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.3e-126;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCGACGAGCGCTCTGCAGACAGAGAGCGC 60
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Db 32 GGGTTCGGGGTTTATTGATTGAATTCGCCGGCGGGAGGCTCTGCAGAGAGAGAGCGC 91
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QY 61 GAGAGATGAGATGGCGAGCGGATTCATTGAGCTGCGGAACAGGGCGCCCTCTGATG 120
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QY 121 TGAAGAAGACTTCCTCGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCAG 180
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QY 181 ATGAATTTGAAGACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
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Db 212 ATGAATTTGAAGACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 271
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QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
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RESULT 6
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LOCUS I96074 1052 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5734022.
ACCESSION I96074
VERSION I96074.1 GI:3940544
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Antibodies to a novel mammalian protein associated with
uncontrolled cell division
JOURNAL Patent: US 5734022-A 1 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..1052
/organism="unknown"
BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN

Query Match 85.6%; Score 761; DB 6; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.3e-126;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGTGGCACGAGAGCCCTCTGCAGACAGAGAGCGC 60
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QY 61 GAGAGATGAGATGGCGAGCGGATTCATTGAGCTGCGGAACAGGGCGCCCTCTGATG 120
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QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
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Ddb	332	GCCTAGAAGTATTGGCAGAAAAGTGTCCGAACCTCAGCATCTAAATTTAAGTGGCAACA	391
Qy	349	AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG	408
Ddb	392	AAATTAAGACCTCAGCACAAATAGAGCCACTGAAAAGTTAGAAAACCTCAAGAGCTTAG	451
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Ddb	452	ACCTTTTCAATTTGGAGGTAAACCACTGAACGACTACCGAGAAAATGTGTTCAAGCTCC	511
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Ddb	512	TCCCGCAACTCACATATCTCGACGGCTATCACCGGACGACAAAGGAGGCCCTGACTCGG	571
Qy	529	ATATTGAGGACACGTGAGAGGCCCTGGATGACGAGGAGGAGGCGGTGAGCATGAGGAGGAGT	588
Ddb	572	ATGCTTGAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	631
Qy	589	ATGATGAAGATGCTCAGGTAGTGAACATCAGGAGGCGGAGGAGGAGGAGGAGGAGGTG	648
Ddb	632	ATGATGAAGATGCTCAGGTAGTGAACACGAGGAGGACGAGGATGAGGAGGAGGAGGAGT	691
Qy	649	AAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGG	708
Ddb	692	AAGAGGAGGACGTGAGTGGAGAGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGG	751
Qy	709	TAGATGGCGAGGAAGATGAAGAAGCTTGGTGAAGAAGAGGGGTCAAGACGCGAAAT	768
Ddb	752	TAGATGACGAGGAAGATGAAGAAGCTTGGTGAAGAAGAGGGGTCAAGACGCGAAAAAC	811
Qy	769	GAGAACCTGAAGATGAGGGAGAGATGATCAGCTAACTAGAATAACCTATTTTGAATAAT	828
Ddb	812	GAGAACCTGAAGATGAGGGAGAGATGATGACTAAGTGAATAACCTATTTTGAATAAT	871
Qy	829	CCTATTGTGATTGACTGTTTTTACCCTATCCCT-----CCCCCTCCCAATCCTGCC	882
Ddb	872	CCTATTGTGATTGACTGTTTTTACCCTATCCCTCTCCCCCCCCCTCTAATCCTGCC	931
Qy	893	CCCTGAA 889	
Ddb	932	CCCTGAA 938	
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326 a 196 c 316 g 214 t			
ORIGIN			
Query Match 85.6%; Score 761; DB 9; Length 1052;			
Best Local Similarity 92.5%; Pred. No. 3.3e-126;			
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;			
Qy	1	GGGTCGAGGTTTATTGATTGGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGAGCGC	60
Db	32	GGGTCGAGGTTTATTGATTGGAATTCGGCGCGGAGCCTCTGCAGAGAGAGCGC	91
Qy	61	GAGAGATGGAGATGGCAGACGGATTTCATTGAGAGCTGCGGAACAGAGGCGCCTCTGTATG	120
Db	92	GAGAGATGGAGATGGCAGACGGATTTCATTGAGAGCTGCGGAACAGAGGCGCCTCTGTATG	151
Qy	121	TGAAAGAACTTCCCTGGGACAAACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG	180
Db	152	TGAAAGAACTTCTCTGGGACAAACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG	211
Qy	181	ATCAATTTCAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCCCTACCTCAATCTCAG	240
Db	212	ATGAATTTCAAGAACTGGAAATTCCTTAAGTAAATCAACGTAGGCTCCTCACTCAATCGCAA	271
Qy	241	ACTTACCAAAAGTTA--AAAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG	288
Db	272	ACTTACCAAAAGTTAACAACACTTAAGAGCTTGAACCTAAGCCTAAGCCTAAGCCTCAGGG	331
Qy	289	GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA	348
Db	332	GCCTGGAAGTATTGGCAGAAAAGTGTCCGAACCTCAGCATCTAAATTTAAGTGGCAACA	391
Qy	349	AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG	408
Db	392	AAATTAAGACCTCAGCACAAATAGAGCCACTGAAAAGTTAGAAAACCTCAAGAGCTTAG	451
Qy	409	ACCTTTTCAATTTGGAGGTAAACCACTGAAACAGTTTAGAAAACCTGTTCAAGCTTC	468
Db	452	ACCTTTTCAATTTGGAGGTAAACCACTGAAACAGTTTAGAAAACCTGTTCAAGCTTC	511
Qy	469	TCCTGCAACTCACATATCTCGACAGCTTTACTTGGGACCAACAGAGAGGCCCTTACTCAG	528
Db	512	TCCCGCAACTCACATATCTCGACGGCTATCACCGGACGACAAAGGAGGCCCTGACTCGG	571
Qy	529	ATATTGAGGACACGTGAGAGGCCCTGGATGACGAGGAGGAGGCGGTGAGCATGAGGAGGAGT	588
Db	572	ATGCTTGAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	631
Qy	589	ATGATGAAGATGCTCAGGTAGTGAACATCAGGAGGCGGAGGAGGAGGAGGAGGAGGTG	648
Db	632	ATGATGAAGATGCTCAGGTAGTGAACACGAGGAGGACGAGGATGAGGAGGAGGAGGAGT	691
Qy	649	AAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGG	708
Db	692	AAGAGGAGGACGTGAGTGGAGAGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGG	751
Qy	709	TAGATGGCGAGGAAGATGAAGAAGCTTGGTGAAGAAGAGGGGTCAAGACGCGAAAT	768
Db	752	TAGATGACGAGGAAGATGAAGAAGCTTGGTGAAGAAGAGGGGTCAAGACGCGAAAAAC	811
Qy	769	GAGAACCTGAAGATGAGGGAGAGATGATCAGCTAACTAGAATAACCTATTTTGAATAAT	828
Db	812	GAGAACCTGAAGATGAGGGAGAGATGATGACTAAGTGAATAACCTATTTTGAATAAT	871
Qy	829	CCTATTGTGATTGACTGTTTTTACCCTATCCCT-----CCCCCTCCCAATCCTGCC	882
Db	872	CCTATTGTGATTGACTGTTTTTACCCTATCCCTCTCCCCCCCCCTCTAATCCTGCC	931
Qy	893	CCCTGAA 889	
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Ddb	272	ACTTACCAAGATTAAACAACCTTAAGAAGCTTGAACTAAGCGATTAACAGAGTCTCAGGGG	331
QY	289	GCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA	348
Ddb	332	GCCTAGAAGTATTGGCAGAAAGTGTCCGAACCTCAGCATCTAAATTTAAGTGGCAACA	391
QY	349	AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTTAGAAAACCTCAAGAGCTTAG	408
Ddb	392	AAATTTAAAGACCTCAGCACAAATAGAGCCACTGAAAAGTTAGAAAACCTCAAGAGCTTAG	451
QY	409	ACCTTTTCAATTGGAGGTACCAACACTGAACGACTACGAGAGAAACGTTGTTCAAGCTTC	468
Ddb	452	ACCTTTTCAATTGGAGGTACCAACCTGAACGACTACCGAGAAATGTGTTCAAGCTCC	511
QY	469	TCCTGCAACTCACATATCTCGACAGCTGTTTACTTGGACACACAGAGAGGCCCTTACTCAG	528
Ddb	512	TCGCGCAACTCACATATCTCGACGGCTATCACCGGACGACAAAGGAGGCCCTGACTCGG	571
QY	529	ATATTGAGGACACGTGAGGCCCTGGATGACGAGAGGAGGGGTGAGATGAGAGGAGAT	588
Ddb	572	ATGCTTGAGGGCTAGCTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAT	631
QY	589	ATGATGAAGATGCTCAGTGTAGAACATCAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGTG	648
Ddb	632	ATGATGAAGATGCTCAGTGTAGAACACGAGGAGGACGAGGATGAGGAGGAGGAGGAGGTG	691
QY	649	AAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGTTATAACGATGGAGAGG	708
Ddb	692	AAGAGGAGGACGTGAGTGGAGAGGAGGAGGAGGATCAAGAAAGTTATAACGATGGAGAGG	751
QY	709	TAGATGGCGAGAGATGAGAGAGAGCTTGGTGAAGAAGAAAGGGGTCAAGACGGAAT	768
Ddb	752	TAGATGACGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGGTCAAGAAGCGAAAAC	811
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QY	829	CCTATTGTGATTGACTGTTTTTACCCTATCCCT-----CCCCCTCCCAATCCTGCC	882
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QY	893	CCCTGAA 889	
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DEFINITION			
ACCESSION			
VERSION			
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SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			

Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R.,
Washington,C., Watlington,S., Williams,G., Williamson,A.,
Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J.,
Zorrilla,S., Kucherlapati,R., Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 164945)
Worley,K.C.
Direct Submission
Submitted (07-FEB-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 164945)
Worley,K.C.
Direct Submission
Submitted (01-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 164945)
Worley,K.C.
Direct Submission
Submitted (05-JUN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 164945)
Worley,K.C.
Direct Submission
Submitted (29-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 164945)
Worley,K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
7 (bases 1 to 164945)
Worley,K.C.
Direct Submission
Submitted (07-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 1, 2001 this sequence version replaced gi:14150337.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of low quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

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----- Project Information
Center project name: I5619
Center clone name: 617_D_22

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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genom
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L24554
Center clone name: 150.L.8

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VERSION	U60823.1		
KEYWORDS	complete cds.		
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REFERENCE	1		
AUTHORS	Li, M., Makkinje, A. and Damuni, Z.		
TITLE	Molecular identification of Ilpp2A, a novel potent heat-stable inhibitor protein of protein phosphatase 2A		

JOURNAL	Biochemistry	35	(22),	6998-7002	(1996)
MEDLINE	96240314				
PUBMED	8679524				
REFERENCE	2	(bases 1 to 750)			
AUTHORS	Li, M., Makkinje, A. and Damuni, Z.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-JUN-1996)				
FEATURES	Cellular & Molecular Physiology,				
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	/protein_id="AAC50570.1"				
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	/translation="MEMGRRHLELRNRTPSDVKELVLDNRSNEKLEGLTDFEEL				
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misc_feature	1..750				
BASE COUNT	260 a	130 c	229 g	131 t	
ORIGIN					
Query Match	72.0%;	Score 640.4;	DB 9;	Length 750;	
Best Local Similarity	92.9%;	Pred. No. 1.1e-104;			
Matches	697;	Conservative 0;	Mismatches 41;	Indels 12;	Gaps 2;
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QY	126	GAACCTTGCCCTGGACACACAGTCGGTCAATGAAGCAAACTCGAAGCCCTCACAGATGAA	185		
Db	61	GAACCTTGCTCGACACACAGTCGGTCAATGAAGCAAACTCGAAGCCCTCACAGATGAA	120		
QY	186	TTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAGACTTA	245		
Db	121	TTTGAAGAACTGGAATTCCTTAAGTAAATCAACGTAGCGCTCACCTCAATCGCAAACTTA	180		
QY	246	CCAAAGTTA--AAGTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGGGCCTG	293		
Db	181	CCAAAGTTTAAACAACAACTTAAGAGCTTGAACATAAGCGATAACAGAGTCTCAGGGGGCCTG	240		
QY	294	GAAGTATTGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAATTT	353		
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QY	354	AAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTT	413		
Db	301	AAAGACCTCAGCACAATAGAGCCACTGAAAAAGTTAGAAAACCTCAGAGCTTAGACCTT	360		
QY	414	TTCAATTGGCAGGTAAACCAACCTGAACGACTACGGAGAAAACGTTGTTCAAGCTTCTCCTG	473		
Db	361	TTCAATTGGCAGGTAAACCAACCTGAACGACTACCGAGAAAATGTGTTCAAGCTCTCCCG	420		
QY	474	CAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAGATATT	533		
Db	421	CAACTCACATATCTCGACGCTATGACCGGAGCACAAAGGAGGCCCTGACTCCGGATGCT	480		
QY	534	GAGGACCACTGGAGGGCCCTGGATGACGAGGAGGAGGATGAGCATGAGGAGGATGATGAT	593		
Db	481	GAGGGCTACTGGAGGGCCCTGGATGATGAGGAGGAGTGAAGATGAGGAGGATGATGAT	540		
QY	594	GAAGATGCTCAGTGTGGAAGATGAGGAGGGCGGAGGAGGAGGAGGAGGAGTGAAGAG	653		
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Db 601 GAGGACGTGAGTGGAGAGGAGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGAT 660
QY 714 GCGAGGAGAGATGAAGAAGAGCCTTGGTGAAGAAGAAAGGGGTCAGAACGCGAAAATGAGAA 773
    | ||||||||||||||| ||||||||||||||| ||||||||||||||| |||||||||||||||
Db 661 GACGAGGAGAGATGAAGAAGAGCCTTGGTGAAGAAGAAAGGGGTCAGAACGCGAAAACGAGAA 720
QY 774 CCTGAAGATGAGGGGAGAGACATGACTAA 803
    ||||||||||||||| ||||||||||||||| |||||||||||||||
Db 721 CCTGAAGATGAGGGGAGAGAGATGACTAA 750
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Search completed: December 8, 2002, 22:38:39
Job time : 1957.82 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 19:14:43 ; Search time 167.801 Seconds
(without alignments)
11930.941 Million cell updates/sec

Title: US-09-591-500-3

Perfect score: 889

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	889	100.0	889	20	AA881537
2	889	100.0	889	21	AAA88239
3	889	100.0	1035	21	AAA88237
4	889	100.0	5785	20	AA881535
5	889	100.0	5785	21	AAA88236
6	761	85.6	1052	17	AAT27712
7	761	85.6	1052	20	AA881536
8	761	85.6	1052	21	AAA88238
9	761	85.6	1052	24	AB844424

10	760.2	85.5	906	21	AAA88240
11	756.2	85.1	916	20	AAV71743
12	742	83.5	1155	23	AA576389
13	640.4	72.0	750	21	AAA15294
14	570.8	64.2	980	17	AAT27713
15	570.8	64.2	980	24	AB199657
16	429.2	48.3	762	13	AAQ21630
17	429.2	48.3	762	17	AA277715
18	297.8	33.5	1371	24	ABK84741
19	296.4	33.3	966	20	AA603114
20	217.4	24.5	1588	22	AAK52226
21	215.2	24.2	3453	23	ABV21871
22	215.2	24.2	3453	23	ABV22959
23	215.2	24.2	3453	23	ABV27701
24	215.2	24.2	3453	23	ABV28791
25	214	24.1	701	23	AA576388
26	193.4	21.8	1863	22	AAH49681
27	173	19.5	628	24	ABQ59657
28	154.2	17.3	186	15	AAQ57449
29	132.6	14.9	147	21	AA20354
30	127.6	14.4	560	24	ABL38556
31	121	13.6	333	21	AAA43216
32	110	12.4	3489	21	AAA30290
33	110	12.4	3489	22	AAF82901
34	110	12.4	3489	24	ABA93487
35	110	12.4	32207	20	AAV73805
36	110	12.4	137507	19	AAV19941
37	109.6	12.3	390	23	AA569541
38	107.6	12.1	16442	18	AA83006
39	105.6	11.9	49999	20	AAZ23891
40	105.6	11.9	49999	20	AAZ23896
41	104.6	11.8	708	23	AA569547
42	104.6	11.8	708	23	AA575461
43	104.2	11.7	303	23	ABL24559
44	103.2	11.6	1050	22	AA21685
45	103.2	11.6	2849	22	AA221684

ALIGNMENTS

RESULT 1

AA881537

ID AAX81537 standard; DNA; 889 BP.

XX AAX81537;

AC AAX81537;

XX 26-AUG-1999 (first entry)

XX Genomic sequence of phosphoprotein 32 variant pp32r2.

DE Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;

XX KW prostatic adenocarcinoma; antineoplastic activity;

XX KW transformation suppression; malignant potential; neuroendocrine;

XX KW neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.

XX OS Homo sapiens.

XX PN WO929906-A2.

XX PD 17-JUN-1999.

XX PF 11-DEC-1998; 98WO-US26433.

XX PR 12-DEC-1997; 97US-0069677.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Brody JR, Kadkol SS, Kochevar GJ, Pasternack GR;

XX DR WPI; 1999-385626/32.

XX PT Phosphoprotein 32 (pp32) related genomic sequences

XX PS Claim 1; Fig 5; 65pp; English.

CC The present sequence represents the genomic sequence of phosphoprotein 32 (pp32) variant pp32r2. The pp32r1 and pp32r2 sequences are associated with cancer in prostate, especially prostatic adenocarcinomas. Normal pp32 exerts antineoplastic activity through suppression of cell transformation. Cancer-associated pp32 variants augment, rather than inhibit, transformation. Determining the presence of a gene encoding residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a diagnostic method for predicting malignant potential of neuroendocrine, neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.

XX SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 100.0%; Score 889; DB 20; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.1e-198;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
DB 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60

QY 61 GAGAGATGGAGATGGCAGACGGATTTCATTTCAGAGCTCGGAAACAGAGCGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGCAGACGGATTTCATTTCAGAGCTCGGAAACAGAGCGCCCTCTGATG 120

QY 121 TGAAGAAGACTTCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAG 180
DB 121 TGAAGAAGACTTCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAG 180

QY 181 ATGAATTTGAAGAACTTGGAAATTTCTTAAGTAAATCAACGGAGGCTCAACCTCAATCTCAG 240
DB 181 ATGAATTTGAAGAACTTGGAAATTTCTTAAGTAAATCAACGGAGGCTCAACCTCAATCTCAG 240

QY 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGCGCTGGAAGTAT 300
DB 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGCGCTGGAAGTAT 300

QY 301 TGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTTAAAGACC 360
DB 301 TGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTTAAAGACC 360

QY 361 TCAGCACAATAGAGCACTGAAACAGTGTAGAAACCTCAAGAGCTTAGACCTTTTCAATT 420
DB 361 TCAGCACAATAGAGCACTGAAACAGTGTAGAAACCTCAAGAGCTTAGACCTTTTCAATT 420

QY 421 GCGAGGTAAACCACTGAAACAGTGTAGAGAAACGTTTCAAGCTTCTCTGCAACTCA 480
DB 421 GCGAGGTAAACCACTGAAACAGTGTAGAGAAACGTTTCAAGCTTCTCTGCAACTCA 480

QY 481 CATATCTCAGAGCTGTACTGGGACCACAGGAGGCCCTTACTCAGATATTGAGGACC 540
DB 481 CATATCTCAGAGCTGTACTGGGACCACAGGAGGCCCTTACTCAGATATTGAGGACC 540

QY 541 ACCTGAGGGCCCTGGATGACGAGGAGGGGTGACCATGAGGAGGTATGATGAAGATG 600
DB 541 ACCTGAGGGCCCTGGATGACGAGGAGGGGTGACCATGAGGAGGTATGATGAAGATG 600

QY 601 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660

QY 661 TGAGTGGAGGGACACGAGGAGGTGAAGAGGTTTAAACATGGAGAGGTAGATGCGGAGG 720
DB 661 TGAGTGGAGGGACACGAGGAGGTGAAGAGGTTTAAACATGGAGAGGTAGATGCGGAGG 720

QY 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAATTCAGAACCTGAAG 780
DB 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAATTCAGAACCTGAAG 780

QY 781 ATGAGGGAAGAGTATGATGACTAAGTAGAATAACCTATTTTTGAATAATTTCCATTGTGATT 840
DB 781 ATGAGGGAAGAGTATGATGACTAAGTAGAATAACCTATTTTTGAATAATTTCCATTGTGATT 840

DB 781 ATGAGGGAAGAGTATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 840

QY 841 TGACTGTTTTTACCACATATCCCTCCCTCCCTCCCTCAATCCTGCCCTGAA 889
DB 841 TGACTGTTTTTACCACATATCCCTCCCTCCCTCCCTCAATCCTGCCCTGAA 889

RESULT 2
ID AAA88239 standard; DNA; 889 BP.
XX AC AAA88239;
XX DT 15-DEC-2000 (first entry)
XX DE Human variant pp32r2 genomic DNA sequence.
XX KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
XX KW malignant; cytostatic; gene therapy; ds.
XX OS Homo sapiens.
XX PN W0200045852-A1.
XX PD 10-AUG-2000.
XX PF 03-FEB-2000; 2000WO-US02656.
XX PR 03-FEB-1999; 99US-0118667.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Pasternack GR, Bai J;
XX WPI; 2000-514896/46.
XX Treatment of cancer comprising restoration of pp32 function in malignant cells -
XX Example 5; Fig 5; 90pp; English.
XX The present invention describes a method (M1) for treating malignant cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an inducer of pp32 expression comprising measuring pp32 expression by cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an inducer of pp32 function comprising measuring protein phosphatase activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents which may be used to treat cancer. Human pp32 is a phosphoprotein which has been mapped to chromosome 15q22.3-q23. The present sequence represents the human variant pp32r2 genomic DNA sequence from an example of the present invention.
XX SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 100.0%; Score 889; DB 21; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.1e-198;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
DB 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60

QY 61 GAGAGATGGAGATGGCAGACGGATTTCATTTCAGAGCTTCGGAACAGAGCGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGCAGACGGATTTCATTTCAGAGCTTCGGAACAGAGCGCCCTCTGATG 120

QY 121 TGAAGAAGACTTCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAG 180
DB 121 TGAAGAAGACTTCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAG 180

Query Match	100.0%	Score	889	DB	21	Length	1035		
Best Local Similarity	100.0%	Pred.	No. 1.le-198						
Matches	889	Conservative	0	Mismatches	0	Indels	0	Gaps	
Qy	1	GGGTCGAGGTTATTGATTGAATTCGGCTCGCAGGAGAGCCCTCGACACAGAGAGCC	60						
Db	32	GGGTCGAGGTTATTGATTGAATTCGGCTCGCAGGAGAGCCCTCGACACAGAGAGCC	91						
Qy	61	GAGAGATGGAGATGGCAGACGAGATTTCATTGAGAGCTCGCGAAACAGGGCCCTCTGATG	120						
Db.	92	GAGAGATGGAGATGGCAGACGAGATTTCATTGAGAGCTCGCGAAACAGGGCCCTCTGATG	151						
Qy	121	TGAAAGAACTTGGCTCGGACACACATCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG	180						
Db	152	TGAAAGAACTTGGCTCGGACACACATCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG	211						
Qy	181	ATGAATTTGAAGAACTGGGAATTTCTTAAGTAAAACTCAACGGAGGCGCTCACCTCAATCTCAG	240						
Db	212	ATGAATTTGAAGAACTGGGAATTTCTTAAGTAAAACTCAACGGAGGCGCTCACCTCAATCTCAG	271						
Qy	241	ACTTACCAAAGTTTAAAGTTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCCTGGAAGTAT	300						
Db	272	ACTTACCAAAGTTTAAAGTTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCCTGGAAGTAT	331						
Qy	301	TGGCAGAAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGCAACAAATTTAAAGACC	360						
Db	332	TGGCAGAAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGCAACAAATTTAAAGACC	391						
Qy	361	TCAGCACAATAGAGCCACCTGAACACAGTTTGAAGAAACCTCAGAGCTTAGACCTTTTCAATT	420						
Db	392	TCAGCACAATAGAGCCACCTGAACACAGTTTGAAGAAACCTCAGAGCTTAGACCTTTTCAATT	451						
Qy	421	GCGAGGTAAACCACTTGAACGACTACGGAGAAAACGTTTCAAGCTTCTCCTGCAACTCA	480						
Db	452	GCGAGGTAAACCACTTGAACGACTACGGAGAAAACGTTTCAAGCTTCTCCTGCAACTCA	511						
Qy	481	CATATCTCGACAGCTGTTTACTGGGACCAACAGGAGGGCCCTTACTCAGATATTTGAGGACC	540						
Db	512	CATATCTCGACAGCTGTTTACTGGGACCAACAGGAGGGCCCTTACTCAGATATTTGAGGACC	571						
Qy	541	ACGTGGAGGCCCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATG	600						
Db	572	ACGTGGAGGCCCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATG	631						

Query Match	100.0%	Score	889	DB	21	Length	1035		
Best Local Similarity	100.0%	Pred.	No. 1.le-198						
Matches	889	Conservative	0	Mismatches	0	Indels	0	Gaps	
Qy	1	GGGTCGAGGTTATTGATTGAATTCGGCTCGCAGAGAGCCCTCGACACAGAGAGCC	60						
Db	32	GGGTCGAGGTTATTGATTGAATTCGGCTCGCAGAGAGCCCTCGACACAGAGAGCC	91						
Qy	61	GAGAGATGGAGATGGCAGACGAGATTTCATTGAGAGCTCGCGAAACAGGGCCCTCTGATG	120						
Db.	92	GAGAGATGGAGATGGCAGACGAGATTTCATTGAGAGCTCGCGAAACAGGGCCCTCTGATG	151						
Qy	121	TGAAGAAGCTTGGCTGGGACACACATCGGTCGAATGAAGGCAACTCGAAGCCCTCACAG	180						
Db	152	TGAAGAAGCTTGGCTGGGACACACATCGGTCGAATGAAGGCAACTCGAAGCCCTCACAG	211						
Qy	181	ATGAATTTGAAGAAGCTGGAATTCCTTAAGTAAAACTCAACGGAGGCGCTCACCTCAATCTCAG	240						
Db	212	ATGAATTTGAAGAAGCTGGAATTCCTTAAGTAAAACTCAACGGAGGCGCTCACCTCAATCTCAG	271						
Qy	241	ACTTACCAAAGTTTAAAGTTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCGCTGGAAGTAT	300						
Db	272	ACTTACCAAAGTTTAAAGTTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCGCTGGAAGTAT	331						
Qy	301	TGGCAGAAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGGCAACAAATTTAAAGACC	360						
Db	332	TGGCAGAAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGGCAACAAATTTAAAGACC	391						
Qy	361	TCAGCACAATAGAGCCACCTGAACAGTGTAGAAACCTTCAGAGCTTAGACCTTTTCAATT	420						
Db	392	TCAGCACAATAGAGCCACCTGAACAGTGTAGAAACCTTCAGAGCTTAGACCTTTTCAATT	451						
Qy	421	GCGAGGTAAACCACTTGAACGACTACGGAGAAAACGTTCTCAAGCTTCTCCTGCAACTCA	480						
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Qy	481	CATATCTCGACAGCTGTTACTGGGACCAACAGAGGGCCCCCTTACTCAGATATTTGAGGACC	540						
Db	512	CATATCTCGACAGCTGTTACTGGGACCAACAGAGGGCCCCCTTACTCAGATATTTGAGGACC	571						
Qy	541	ACGTGGAGGCCCTGGATGACGAGGAGGGGTGACCATGAGGAGGATATGATGAAGATG	600						
Db	572	ACGTGGAGGCCCTGGATGACGAGGAGGGGTGACCATGAGGAGGATATGATGAAGATG	631						

malignant; cytostatic; gene therapy; ds.
Homo sapiens.
WO200045852-A1.
10-AUG-2000.
03-FEB-2000; 2000WO-US02656.
03-FEB-1999; 99US-0118667.
(UYJO) UNIV JOHNS HOPKINS.
Pasternack GR, Bai J;
WPI; 2000-514896/46.
Treatment of cancer comprising restoration of pp32 function in
malignant cells -
Example 3; Fig 2; 90pp; English.
The present invention describes a method (M1) for treating malignant
cells comprising restoration of pp32 function. Also described are:
(1) a method (M2) of screening to determine whether a compound is an
inducer of pp32 expression comprising measuring pp32 expression by
cells cultured in the presence and absence of the compound; and
(2) a method (M3) of screening to determine whether a compound is an
inducer of pp32 function comprising measuring protein phosphatase
activity in cells cultured in the presence and absence of the compound.
The methods are useful for treating cancer and for identifying agents
which may be used to treat cancer. Human pp32 is a phosphoprotein which
has been mapped to chromosome 15q22.3-q23. The present sequence
represents the human placenta variant pp32rl genomic DNA sequence from
an example of the present invention.
Sequence 5785 BP; 1755 A; 1087 C; 1162 G; 1781 T; 0 other;
Query Match 100.0%; Score 889; DB 21; Length 5785;
Best Local Similarity 100.0%; Pred. No. 2e-198;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 GAGAGATGGAGATGGCGACGCGGATTCATTTCAGAGCTCGCGAACAGAGCGCCCTCTGTATG 120
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Qy 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAG 240
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Qy 241 ACTTACCAAGTTAAAGTTGAGAAGCTTGAACCTAAGAGTCTCAGGGGGCTTGGAAAGTAT 300
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Db TGGCAGAAAGTGTCCTCAAACTCAGCATCTATATTTAAGTGGCAACAAATTAAGAGACC 4747
Qy 361 TCAGCAACAATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAGAGCTTTTCAATT 420
Db TCAGCAACAATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAGAGCTTTTCAATT 4807
Qy 421 GCGAGGTAAACCACTGAAGAGCTTACGGAGAAACAGTGTTCAGGCTTCTCCTGCAACTCA 480

Db 4808 GCGAGGTAAACCACTGAAGAGCTACGGAGAAACAGTGTTCAGGCTTCTCCTGCAACTCA 4867
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Qy 541 ACCTGAGGGCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGATGATGATGAAGATG 600
Db ACCTGAGGGCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGATGATGATGAAGATG 4987
Qy 601 CTCAGGTAGTGAAGATGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db CTCAGGTAGTGAAGATGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Qy 661 TGAGTGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGAGAGGTAGATGCGGAGG 720
Db TGAGTGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGAGAGGTAGATGCGGAGG 5107
Qy 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAATGAGAACCTGAAG 780
Db AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAATGAGAACCTGAAG 5167
Qy 781 ATGAGGAGAAAGATGATGACTAAGTAGATAACCTATTTTGAAGAAATTCCTATTGTGATT 840
Db ATGAGGAGAAAGATGATGACTAAGTAGATAACCTATTTTGAAGAAATTCCTATTGTGATT 5227
Qy 841 TGACTGTTTTTACCCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 889
Db TGACTGTTTTTACCCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 5276
RESULT 6
AAT27712
ID AAT27712 standard; cDNA; 1052 BP.
XX
AC AAT27712;
XX
DT 30-JUL-1996 (first entry)
XX
DE Human pp32 cDNA.
XX
KW pp32; cancer; diagnosis; therapy; antisense; cell proliferation;
KW lymphoid tumour; epithelial tumour; colon carcinoma;
KW prostate carcinoma; non-Hodgkin lymphoma; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 97..846
FT /*tag= a
XX
PN WO9610092-A1.
XX
PD 04-APR-1996.
XX
PF 28-SEP-1995; 95WO-US12414.
XX
PR 28-SEP-1994; 94US-0314503.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Kuhajda FP, Pasternack GR;
XX
DR WPI; 1996-200930/20.
DR P-PSDB; AAR95900.
XX
PT New method of diagnosing cancer using pp32 cDNA - by detecting the
PT level of mRNA hybridising to pp32 cDNA; also for inhibiting cell
XX proliferation and screening anti-cancer drugs.
PS Claim 1; Fig 10a; 129pp; English.
XX
CC Human cDNA (AAT27712) cloned from HL-60 cells codes for a 32 kDa

Db 212 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAACGTAGGCCTCACCTCAATCGCAA 271
Qy 241 ACTTACCAAACTTA---AAGTTGAGAAGCTTGAACTA-----AGAGTCTCAGGGG 288
Db 272 ACTTACCAAACTTAACAACTTAAGAGCTTGAACTAAGGATAACAGAGTCTCAGGGG 331
Qy 289 GCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGGCATCTATATTTAAGTGGCAACA 348
Db 332 GCCTAGAAGTATTGGCAGAAAGTGTCCGAACCTCAGGCATCTAAATTTAAGTGGCAACA 391
Qy 349 AAATTAAGACCTCAGCACATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 392 AAATTAAGACCTCAGCACATAGAGCCACTGAAAAAAGTTAGAAAACCTCAAGAGCTTAG 451
Qy 409 ACCTTTTCAATTTGGAGTAGTACCAACCTGAAACGACTACGGAGAAACGTTCTCAAGCTTC 468
Db 452 ACCTTTTCAATTTGGAGTAGTACCAACCTGAAACGACTACGGAGAAATGTGTCAAGCTTC 511
Qy 469 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCAG 528
Db 512 TCCCGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCAG 571
Qy 529 ATATTGAGGACCACTGAGAGGCTGTGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGT 588
Db 572 ATGCTGAGGCTACGTGAGGAGGCTGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGT 631
Qy 589 ATGATGAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 648
Db 632 ATGATGAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 691
Qy 649 AAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
Db 692 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 751
Qy 709 TAGATGGCAGGAGAGTGAAGAAGAGCTTGGTGAAGAAGAAGAGGAGGAGGAGGAGGAGT 768
Db 752 TAGATGACGAGGAGAGTGAAGAAGAGCTTGGTGAAGAAGAAGAGGAGGAGGAGGAGT 811
Qy 769 GAGAACCTGAGATGAGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
Db 812 GAGAACCTGAGATGAGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 871
Qy 829 CCTATTGTGATTTGACTGTTTTTACCCTATATCCCT-----CCCCCTTCCATCTGCC 882
Db 872 CCTATTGTGATTTGACTGTTTTTACCCTATATCCCTTCCCTCCCTCCCTTCCCTTCCCT 931
Qy 883 CCCTGAA 889
Db 932 CCCTGAA 938

RESULT 8
ID AAA88238 standard; DNA; 1052 BP.
AC AC
AA88238;
DT 15-DEC-2000 (first entry)
XX Human pp32 nucleotide sequence.
XX
XX Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX WO200045852-A1.
XX
XX 10-AUG-2000.
PD
XX 03-FEB-2000; 2000WO-US02656.
XX
XX

PR 03-FEB-1999; 99US-0118667.
XX (UYJO) UNIV JOHNS HOPKINS.
PA Pasternack GR, Bai J;
PI WPI; 2000-514896/46.
XX P-PSDB; AAB20656.
DR Treatment of cancer comprising restoration of pp32 function in
XX malignant cells -
PT Example 3; Fig 3; 90pp; English.
XX
CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human pp32r1 nucleotide sequence from an example of
CC the present invention.
XX
SQ Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;

Query Match 85.6%; Score 761; DB 21; Length 1052;
Best Local Similarity 92.5%; Pred. No. 1.1e-168;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
Db 32 GGGTTCGGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGAGAGAGCGC 91
Qy 61 GAGAGATGAGATGGCGACACGGATTCATTAGAGTCTGGGAACAGGCGCCCTCTGATG 120
Db 92 GAGAGATGAGATGGCGACACGGATTCATTAGAGTCTGGGAACAGGCGCCCTCTGATG 151
Qy 121 TGAAGAACTTCGCCGTGGACAAACAGTCGCTCGAATGAAGGCAAACTTCGAAGCCCTCACAG 180
Db 152 TGAAGAACTTCGCTGGACAAACAGTCGCTCGAATGAAGGCAAACTTCGAAGCCCTCACAG 211
Qy 181 ATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAG 240
Db 212 ATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACCTAGGCGCTCACCTCAATCGCA 271
Qy 241 ACTTACCAAACTTA---AAGTTGAGAACTTTGAACTA-----AGAGTCTCAGGGG 288
Db 272 ACTTACCAAACTTAACAACTTAAGAGCTTGAACTAAGGATAACAGAGTCTCAGGGG 331
Qy 289 GCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGGCATCTATATTTAAGTGGCAACA 348
Db 332 GCCTAGAAGTATTGGCAGAAAGTGTCCGAACCTCAGGCATCTAAATTTAAGTGGCAACA 391
Qy 349 AAATTAAGACCTCAGCACATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 392 AAATTAAGACCTCAGCACATAGAGCCACTGAAAAAAGTTAGAAAACCTCAAGAGCTTAG 451
Qy 409 ACCTTTTCAATTTGGAGTAGTACCAACCTGAAACGACTACGGAGAAACAGTGTTCAGAGCTTC 468
Db 452 ACCTTTTCAATTTGGAGTAGTACCAACCTGAAACGACTACGGAGAAATGTGTTCAGAGCTTC 511
Qy 469 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCAG 528
Db 512 TCCCGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCAG 571
Qy 529 ATATTGAGGACCACTGAGAGGCGCTGTGATGACGAGGAGGAGGAGGAGGAGGAGGAGT 588
Db 572 ATGCTGAGGCTACGTGAGGAGGCGCTGTGATGATGAGGAGGAGGAGGAGGAGGAGT 631

XX WO200175067-A2.
PN 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI WPI: 2001-639362/73.
XX P-PSDB; ABG12202.
DR
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 12193; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS4197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1155 BP; 340 A; 219 C; 347 G; 249 T; 0 other;

Query Match 83.5%; Score 742; DB 23; Length 1155;
Best Local Similarity 91.9%; Pred. No. 3.3e-164;
Matches 834; Conservative 0; Mismatches 55; Indels 19; Gaps 4;

Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCACACGAGAGCCCTCTCGACAGACAGAGCGC 60
Dy 57 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGCGGGAGCGCTCTCGACAGAGAGAGCGC 116
Qy 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGCGAACAGCGGCCCTCTCGATG 120
Dy 117 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGCGAACAGCGGCCCTCTCGATG 176
Qy 121 TGAAGAACTTGCCTCGACAACTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Dy 177 TGAAGAACTTGTCTCGACAACTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 236
Qy 181 ATGAATTGGAAGACTGGAATTCCTTAAGTAAATCAACAGGAGCGCTCACCTCAATCTCAG 240
Dy 237 ATGAATTGGAAGAACTGGAATTCCTTAAGTAAATCAACAGTGGCCTCACCTCAATCGCAA 296
Qy 241 ACTTACCACAACTTA--AAGTTGAGAAGCTTGAACATA-----AGAGTCTCAGGG 288
Dy 297 ACTTACCACAACTTAAGAAAGCTTGAAGAGCTTGAACATAAGCGATAACAGAGAGTCTCAGGG 356
Qy 289 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGG-CATCTATATTAAAGTGGCAAC 347

Db 357 GCCTGGAAGTATTGGCAGAAAAGTGTCCGAACCTTCGCCCATCTAATTTAAGGTGCAAC 416
Qy 348 AAAATTAAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTA 407
Dy 417 AAAATTAAAGACCTCAGCACAATAGAGCCACTTGGAAAAGTTAGAAAACCTCAAGAGCTTA 476
Qy 408 GACCTTTTCAATTGCGAGGTAAACCACTGAACGACTACGGAGAAAACCTGTTCAAGCTT 467
Dy 477 GACCTTTTCAATTGCGAGGTAAACCACTGAACGACTACGGAGAAAATGTTTCAAGCTC 536
Qy 468 CTCTCTCAACTACATATCTCGACAGCTGTACTGGGACCAACAAGGAGGCCCTTACTCA 527
Dy 537 CTCTCCCACTACATATCTCGACGCTATGACCGGAGCAGCAAGGAGGCCCTGACTCG 596
Qy 528 GATATTGAGGACACGCTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAG 587
Dy 597 GATGCTGAGGGCTACGCTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 656
Qy 588 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 647
Dy 657 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGATGAGGAGGAGGAGT 716
Qy 648 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTATAACGATCGAGAG 707
Dy 717 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGATGAAGAAGTTATAACGATCGAGAG 776
Qy 708 GTAGATGGGAGGAGGAGGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGCGAAA 767
Dy 777 GTAGATGACGAGGAGGAGGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGCGAAA 836
Qy 768 TGGAACCTTGAAGATGAGGAGGAGGAGGATGATGACTAAGTAGAATTAACCTATTTTGA 827
Dy 837 CGAAGACCTTGAAGATGAGGAGGAGGAGGATGATGACTAAGTAGAATTAACCTATTTTGA 896
Qy 828 TCCTATTGTGATTGACTGTTTACCCTATATCCCT-----CCCCCTCCAATCCTCGC 881
Dy 897 TCCTATTGTGATTGACTGTTTACCCTATATCCCTCTCCCCCCCCCTCCCAATCCTCGC 956
Qy 882 CCCCTGAA 889
Dy 957 CCCCTGAA 964

RESULT 13
ID AAA15294 standard; cDNA; 750 BP.
XX AC AAA15294;
XX AC AAA15294;
DT 04-SEP-2000 (first entry)
XX
DE cDNA encoding a protein phosphatase 2A inhibitor.
XX
KW Syndecan-4; angiogenesis; proteoglycan; protein kinase C;
KW delta-isoenzyme; alpha isoenzyme; protein phosphatase; infarction;
KW endothelial cell proliferation; endothelial cell migration; anoxia;
KW myocardial infarction; chronic myocardial ischemia; heart tissue; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..750
FT /*tag= a
XX
XX WO200027416-A1.
XX
XX 18-MAY-2000.
XX
XX 10-NOV-1999; 99WO-US26647.
XX
XX 12-NOV-1998; 98US-0190976.
XX

Db 10 AGAGAGCGCGAGAGATGGAGATGGACAAACGGATTATTTAGAGCTCGGAACAGGAC 69
Qy 110 GCCCTCTGATGTGAAGAACTTGCCTGGACACACAGTCGTCGTAATCAAGGCAAACTCGA 169
Db 70 GCCCTCTGATGTGAAGAGCTGGTCCCTGGATAGTCTGTAAGTCAATTGAAGGCAAAATCGA 129
Qy 170 AGCCCTCACAGATGAATTTGAAGAACTTGAATTTCTTAAGTAAATCAACGAGGCGCTCAC 229
Db 130 AGGCTCACGGATGAGTTTGAGAACTTGAATTTCTTAAGTCAATCAACGTAGGCTCAC 189
Qy 230 CTCATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 277
Db 190 CTCATTTTCCAACCTTAGCAAAAGTTAAACAACCTCAAGAAAGCTTGAATTAAGCGAAACAG 249
Qy 278 AGTCTCAGGGGCGCTGAACTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTT 337
Db 250 AATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCATCTAAATTT 309
Qy 338 AAGTGGCAACAAATTAAGAACCTTCAGCAACAATAGAGCCACTGAACAGTTAGAAAACCT 397
Db 310 AAGTGGCAACAATAAAGATCTCAGCAACAATAGAGCCGCTGAAGAACTTAGAGATCT 369
Qy 398 CAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCAACCTGAACGACTACGAGAAACGT 457
Db 370 CAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCAACCTGAACGACTACGAGAAACGT 429
Qy 458 GTTCAAGCTTCTCTGCAATCTACATATCTCGACAGCTGTACTGGGACCACAGAGGC 517
Db 430 GTTCAAGCTTCTCTGCAATCTACATATCTCGACAGCTGTACTGGGACCACAGAGGC 489
Qy 518 CCCTTACTCAGATATTGAGGACCAACGCTGGAGGCGCTGGATCAGGAGGAGGCTGAGCA 577
Db 490 CCCGACTCCGATGTTGAGGCTACGTGGA-----GGATGACGACGAGGAATGAGGA 543
Qy 578 TGAGGAGGATGATGATGAAGATGCTCAGGTAGTGGAGAGATGAGGAGGCGGAGGAGGA 637
Db 544 TGAGGAGGATGATGATGAATATGCCAGCTAGTGGAAAGATGAAGAGGAGGCTTGAGGA 603
Qy 638 GGAGAAAGGTGAAGAGGAGGAGCTGAGTGGAGGCGGAGGAGGATCAAGAGGTTATTA 697
Db 604 GGAAGAGGGGAGGAAGAGGATGTGAGTGGAGGAGGAGGAGGATGAGGAAGGTTACAA 663
Qy 698 CGATGGAGAGGTAGATGGCGAGGAAGATGAAGAGAGCTTGGTGAAGAAAGGCGTCA 757
Db 664 TGACGGGAACTGATGATCAGGAGGAGACGAGAGAGCTGGTGAAGAGAGGAGGATCA 723
Qy 758 GAAGCGAAATGAGAACTTGAAGATGAGGAGGAGAGATGATGACTTAAGTGAATTAACCTAT 817
Db 724 GAAGCGAAACGAGAACCGGACGATGAGGCGGAAGAGGATGACTTAAGGA-ATCAACCTGT 782
Qy 818 TTTGAAATAATCTTATTTGATTTGATTTGACTGTTTTTACCCTATATCCCTCCCTCCCAATC 877
Db 783 TTGGGAAATTCCTTATTTGATTTGATTTGACTGTTTTTACCCTATATCCCTCCCTCCCTATTC 842
Qy 878 CTGCCCCCTGAA 889
Db 843 CTGCCCCCGGAA 854

RESULT 15
ABI99657
ID ABI99657 standard; cDNA; 980 BP.
XX
AC ABI99657;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:687.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX

OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP04192.
XX
PR 18-MAY-2000; 2000JP-0145977.
XX
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
WPI: 2002-034733/04.
DR P-PSDB; ABB57251.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
PS Claim 2; Page 1714-1716; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC the expression levels of particular genes (ABI99202 to ABI99912, encoding
CC the protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischaemic condition-improving
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 980 BP; 312 A; 169 C; 302 G; 197 T; 0 other;

Query Match 64.2%; Score 570.8; DB 24; Length 980;
Best Local Similarity 82.9%; Pred. No. 4e-124;
Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;
Qy 50 ACAGAGCGCGAGAGATGGAGATGGCGAGACGAGATTCATTGAGAGCTGCGGAACAGGCG 109
Db 10 AGAGAGCGCGAGAGATGGAGATGGCAACAGGATTTATTTAGAGCTGCGGAACAGGAC 69
Qy 110 GCCCTCTGATGTGAAGAACTTGCCTGGACACACAGTCGGTCAATGAGGCAAACTCGA 169
Db 70 GCCCTCTGATGTGAAGAGCTGCTCTGGATAACTGTAGTCAATGAGGCAAAATCGA 129
Qy 170 AGCCCTCACAGATGAATTTGAAGAACTTGAATTTCTTAAGTAAATCAACGAGGCGCTCAC 229
Db 130 AGGCTCACGGATGAGTTTGAGAACTGGAATTCCTTGAATCAATCAACGTAGGCTCAC 189
Qy 230 CTCATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 277
Db 190 CTCATTTTCCAACCTTAGCAAAAGTTAAACAACCTCAAGAAAGCTTGAATTAAGCGAAACAG 249
Qy 278 AGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTT 337
Db 250 AATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCATCTAAATTT 309
Qy 338 AAGTGGCAACAAATTAAGAACTTCAGCAACAATAGAGCCACTGAACAGTTAGAAAACCT 397
Db 310 AAGTGGCAACAATAAAGATCTCAGCAACAATAGAGCCGCTGAAGAACTTAGAGATCT 369
Qy 398 CAAGAGCTTAGACCTTTTCAATTTGGCAGGTAAACCAACCTTGAACGACTACGGAAGAAACGT 457
Db 370 CAAGAGCTTAGACCTTGTTTAACTGTGAGGTGACCAACCTGGAATGCTTACCAGAGAAACGT 429

Qy	458	GTTCAAAGCTTCTCCTGCAACTCACATATCTCGACAGCTGTTACTGGACCAACAAGGAGGC	517
Db	430	GTTCAAAGCTCCTGCCCGGCTCATGTACCTCGATGGCTATGACAGGGACAACAAGGAGGC	489
Qy	518	CCCTTACTCAGATATTGAGGACCACGTGGAGGGCTGGATGACGAGGAGGGGTGAGCA	577
Db	490	CCCCGACTCCGATGTTGAGGGCTACGTGGA-----GGATGACGACGAGGAAAGATGAGGA	543
Qy	578	TGAGGAGGATATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGCAGGAGGAGGA	637
Db	544	TGAGGAGGATATGATGAATATGCCAGCTAGTGGAGATGAAGAGGAAGGTTGAGGA	603
Qy	638	GGAGGAAGGTGAAGAGGAGGACGTGAGTGGAGGGACGAGGAGATGAAGAAGCTTATAA	697
Db	604	GGAGAAGGGGAGGAAGAGGATGTGAGTGGAGAGGAGGAGGAGGATGAGGAAGGTTACAA	663
Qy	698	CGATGGAGAGGTAGATGCGGAGGAGAGATGAAGAAGCTTGGTGAAGAAGAAAGGGGTCA	757
Db	664	TGACGGGGAAGTGGATGACGAGGAAGACGAAGAAGCTGGTGAAGAAGAAAGGGAGTCA	723
Qy	758	GAAGCGAAATGAGAACTGAGAGATGAGGGAGAAAGATGATGACTAAGTAGAATAACCTAT	817
Db	724	GAAGCGAAACGAGAACCGGACGATGAGGGCGAAGAGGATGACTAAGGA-ATGAACCTGT	782
Qy	818	TTTGAAAAATTCCTATTGCTGATTTGACTGTTTACCATATCCCTCCCTCCCTCCCAATC	877
Db	783	TTGGGGAATTCCTATTGCTGATTTGACTGTTTACCATATCCCTCCCTCCCTCCCTATTC	842
Qy	878	CTGCCCCCTGAA	889
Db	843	CTGCCCCCGGAA	854

Search completed: December 8, 2002, 21:37:52
Job time : 180.801 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:29:48 ; Search time 37.6192 Seconds
(without alignments)
7247.256 Million cell updates/sec

Title: US-09-591-500-3

Perfect score: 889

Sequence: 1 gggttcgagttattgatt.....ctccaatctgccccctgaa 889

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2.6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	761	85.6	1052	1 US-08-466-603-1	Sequence 1, Appli
2	761	85.6	1052	1 US-08-314-503A-1	Sequence 1, Appli
3	761	85.6	1052	1 US-08-468-066-1	Sequence 1, Appli
4	761	85.6	1052	2 US-08-466-717-1	Sequence 1, Appli
5	761	85.6	1052	3 US-08-466-743-1	Sequence 1, Appli
6	761	85.6	1052	5 PCT-US95-12414-1	Sequence 1, Appli
7	570.8	64.2	980	1 US-08-466-603-3	Sequence 3, Appli
8	570.8	64.2	980	1 US-08-314-503A-3	Sequence 3, Appli
9	570.8	64.2	980	1 US-08-468-066-3	Sequence 3, Appli
10	570.8	64.2	980	2 US-08-466-717-3	Sequence 3, Appli
11	570.8	64.2	980	3 US-08-466-743-3	Sequence 3, Appli
12	570.8	64.2	980	5 PCT-US95-12414-3	Sequence 3, Appli
13	429.2	48.3	759	1 US-08-466-603-4	Sequence 4, Appli
14	429.2	48.3	759	1 US-08-314-503A-4	Sequence 4, Appli
15	429.2	48.3	759	1 US-08-468-066-4	Sequence 4, Appli
16	429.2	48.3	759	2 US-08-466-717-4	Sequence 4, Appli
17	429.2	48.3	759	3 US-08-466-743-4	Sequence 4, Appli
18	429.2	48.3	759	5 PCT-US95-12414-4	Sequence 4, Appli
19	296.4	33.3	966	2 US-08-766-738-2	Sequence 2, Appli
20	296.4	33.3	966	4 US-09-262-610-2	Sequence 2, Appli
21	110	12.4	3489	2 US-08-728-323A-1	Sequence 1, Appli
22	110	12.4	3489	4 US-09-298-568-1	Sequence 1, Appli
23	110	12.4	32207	2 US-08-770-379-20	Sequence 20, Appl
24	110	12.4	32207	4 US-08-757-669A-20	Sequence 20, Appl
25	110	12.4	32207	4 US-09-230-371A-20	Sequence 20, Appl
26	107.6	12.1	16442	3 US-08-781-891-208	Sequence 208, App
27	105.2	11.8	7218	1 US-08-232-463-14	Sequence 14, Appl

c 28	102.4	11.5	1926	4 US-09-249-585A-4	Sequence 4, Appli
c 29	102.4	11.5	1931	2 US-09-130-114-2	Sequence 2, Appli
30	94.6	10.6	3211	2 US-08-574-959A-8	Sequence 8, Appli
31	94.6	10.6	3211	4 US-09-357-014-8	Sequence 8, Appli
32	94.6	10.6	3901	2 US-08-574-959A-6	Sequence 6, Appli
33	94.6	10.6	3901	4 US-09-357-014-6	Sequence 6, Appli
c 34	86.2	9.7	51259	3 US-08-781-891-209	Sequence 209, App
35	86.2	9.7	9636	1 US-08-323-170B-1	Sequence 1, Appli
36	86.2	9.7	9636	4 US-08-954-441-1	Sequence 1, Appli
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39	78	8.8	2518	4 US-09-433-699-3	Sequence 3, Appli
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c 42	78	8.8	5452	2 US-09-130-114-1	Sequence 1, Appli
43	78	8.8	9600	4 US-08-910-647-1	Sequence 1, Appli
44	78	8.8	9600	4 US-09-620-925-1	Sequence 1, Appli
45	78	8.8	10596	1 US-07-884-811-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-466-603-1
; Sequence 1, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
US-08-466-603-1

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Query Match      85.6%; Score 761; DB 1; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

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Qy 61 GAGAGATGGAGATGGCGAGAGGATTCATTACAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120
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Qy 121 TGAAGAAGCTTGGCCCTGGACACAGTCGGTTCGAATGAAGCAAACTCGAAGCCCTCACAG 180
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Db 572 ATGCTGAGGAGGCTACGTGAGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAT 631

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Db 752 TAGATGGCGAGGAAGATGAAGAGAGCTTGTGTAAGAGAAGAGGGGTGAGAGCGAAAC 811

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Qy 829 CCTATTGATGATTGACTGTTTTTACCCATATCCCT-----CCCCCTCCAAATCCTGCC 882
Db 872 CCTATTGATGATTGACTGTTTTTACCCATATCCCTCTCCCCCCCCCTCTAAATCCTGCC 931

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RESULT 2
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; Sequence 1, Application US/08314503A
; Patent No. 5734022

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; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-314-503A-1

Query Match      85.6%; Score 761; DB 1; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTAATTCGGCTGGCGACGAGAGCCCTCTGCAGACAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTAATTCGGCGCGCGGAGCCCTCTGCAGAGAGAGAGCGC 91

Qy 61 GAGAGATGGAGATGGCGAGAGGATTCATTACAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120
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Qy 121 TGAAGAAGCTTGGCCCTGGACACAGTCGGTTCGAATGAAGCAAACTCGAAGCCCTCACAG 180
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Qy 529 ATATTGAGGACCACTGAGGAGGCGCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGAT 588
Db 572 ATGCTGAGGAGGCTACGTGAGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAT 631

Qy 589 ATGATGAAGATCCTCAGCTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGG 648
Db 632 ATGATGAAGATCCTCAGCTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGG 691

Qy 649 AAGAGGAGGACGTGAGTGGAGGAGGACGAGGAGGATGAAGAGGTTATAACGATGGAGG 708
Db 692 AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGATGAAGAGGTTATAACGATGGAGG 751

Qy 709 TAGATGGCGAGGAAGATGAAGAGAGCTTGTGTAAGAGAAGAGGGGTGAGAGCGAAAT 768
Db 752 TAGATGGCGAGGAAGATGAAGAGAGCTTGTGTAAGAGAAGAGGGGTGAGAGCGAAAC 811

Qy 769 GAGAAGCTTGAAGATGAGGAGGAAGATGATGACTAAGTGAATAACCTATTTTGAAGAAAT 828
Db 812 GAGAAGCTTGAAGATGAGGAGGAAGATGATGACTAAGTGAATAACCTATTTTGAAGAAAT 871

Qy 829 CCTATTGATGATTGACTGTTTTTACCCATATCCCT-----CCCCCTCCAAATCCTGCC 882
Db 872 CCTATTGATGATTGACTGTTTTTACCCATATCCCTCTCCCCCCCCCTCTAAATCCTGCC 931

Qy 883 CCTGAA 889
Db 932 CCTGAA 938
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Db 872 CCTATTGATTTGACTGTTTTTACCATATCCCTCTCTCCCCCTCTATCCCTGCC 931
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RESULT 3
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; Sequence 1, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kubaide, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-468-066-1

Query Match 85.6%; Score 761; DB 1; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

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QY 409 ACCTTTTCAATTGCGAGGTAAACCACTGAAGGAGTACGAGAGAAAACGTGTTCAAGCTTC 468
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Db 752 TAGATGACGAGGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAGGAGGAGT 811
QY 769 GAGAACTGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 828

Db 812 GAGAACCTGAAGATGAGGAGAGATGATGACTAAGTGAATAACCTATTTTGAATAATT 871
QY 829 CCTATTGTGATTGACTGTTTACCCATATCCCT-----CCCCCTCCAAATCCTGCC 882
Db 872 CCTATTGTGATTGACTGTTTACCCATATCCCTCTCCCTCCCTCTAATCCTGCC 931
QY 883 CCCTGAA 889
Db 932 CCCTGAA 938
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; Sequence 1, Application US/08466717
; Patent No. 5874234
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.717
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-466-717-1
Query Match 85.6%; Score 761; DB 2; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;
QY 1 GGTTTCGAGGTTTATGATTGAATTCGGTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
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QY 883 CCCTGAA 889
Db 932 CCCTGAA 938
RESULT 5
US-08-466-743-1
; Sequence 1, Application US/08466743
; Patent No. 6040173
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia

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Db	572	ATGCTGAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	631
QY	589	ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGGCCGAGGAGGAGGAGGAGGAGGTG	648
Db	632	ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGGACGAGGAGGAGGAGGAGGAGT	691
QY	649	AAGAGGAGGAGCTGATGAGGAGGGACGAGGAGGATGAAGAAGTTATACGATGAGGAGG	708
Db	692	AAGAGGAGGAGCTGATGAGGAGGAGGAGGAGGATGAAGAAGTTATACGATGAGGAGG	751
QY	709	TAGATGCGAGGAAGATGAAGAAGAGCTTGGTGAAAGAAAGGGGTGAGAAGCGAAAT	768
Db	752	TAGATGAGGAGGAAGATGAAGAAGAGCTTGGTGAAAGAAAGGGGTGAGAAGCGAAAC	811
QY	769	GAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAACCTATTTTGAATAAT	828
Db	812	GAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAACCTATTTTGAATAAT	871
QY	829	CCATATGATTTGACTGTTTTTACCCATATCCCT-----CCGCCCTCCAACTCCTGCC	882
Db	872	CCATATGATTTGACTGTTTTTACCCATATCCCTCTCCGCCCTCTATCTCTATCTGCC	931
QY	883	CCCTGAA 889	
Db	932	CCCTGAA 938	
RESULT 6			
PCT-US95-12414-1			
: Sequence 1, Application PC/TUS9512414			
: GENERAL INFORMATION:			
: APPLICANT: Pasternack, Gary R.			
: APPLICANT: Kuhajda, Francis P.			
: TITLE OF INVENTION: Novel Mammalian Protein Associated With			
: TITLE OF INVENTION: Uncontrolled Cell Division			
: NUMBER OF SEQUENCES: 9			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Banner & Allegretti, Ltd.			
: STREET: 1001 G Street, N.W.			
: CITY: Washington, D.C.			
: STATE: District of Columbia			
: COUNTRY: U.S.A.			
: ZIP: 20001			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PatentIn Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: PCT/US95/12414			
: FILING DATE:			
: CLASSIFICATION:			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 08/314,503			
: FILING DATE: 22-SEP-1994			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Hoscheit Esq., Dale H.			
: REGISTRATION NUMBER: 19,090			
: REFERENCE/DOCKET NUMBER: 1107.51507			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: 202 508-9153			
: TELEFAX: 202 508-9299			
: INFORMATION FOR SEQ ID NO: 1:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 1052 base pairs			
: TYPE: nucleic acid			
: STRANDEDNESS: double			
: TOPOLOGY: linear			
: MOLECULE TYPE: cDNA			

; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97...843
; PCT-US95-12414-1

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Query Match      85.6%; Score 761; DB 5; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172; Indels 18; Gaps 3;
Matches 839; Conservative 0; Mismatches 50;

QY 1 GGGTTCGAGTTTATTGATTGAATTCGGCTGGCAGCAGAGAGCCCTCTGCAGACAGAGAGCGC 60
DB 32 GGGTTCGGGGTTTATTGATTGAATTCGCCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCAGACAGGATTCATTAGAGCTCGGAAACAGAGCGCCCTCTGATG 120
DB 92 GAGAGATGAGATGGCAGACAGGATTCATTAGAGCTCGGAAACAGAGCGCCCTCTGATG 151
QY 121 TGAAGAACTTCCCTTGGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCAAG 180
DB 152 TGAAGAACTTCTCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCAAG 211
QY 181 ATGAATTTGAAGAACTTGAATTTTAAAGTAAATCAACGGAGCGCTCACTCAATCTCAG 240
DB 212 ATGAATTTGAAGAACTTGAATTTTAAAGTAAATCAACGGTAGCGCTCACTCAATCGCA 271
QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
DB 272 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 331
QY 289 GCGTGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACA 348
DB 332 GCGTGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACA 391
QY 349 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGCTTAGAAAACTCAAGAGCTTAG 408
DB 392 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGCTTAGAAAACTCAAGAGCTTAG 451
QY 409 ACCTTTTCAATTCGAGGTAACCACTGAACGACTACGGAGAAAACTGTTCAGAGCTTC 468
DB 452 ACCTTTTCAATTCGAGGTAACCACTGAACGACTACGGAGAAAACTGTTCAGAGCTTC 511
QY 469 TCCTGAACCTCACATATCTCGACAGTGTGTACTGGGACCAACAGGAGGCCCTTACTCAG 528
DB 512 TCCTGAACCTCACATATCTCGACAGTGTGTACTGGGACCAACAGGAGGCCCTTACTCAG 571
QY 529 ATATTGAGGACACCTGAGAGGCCCTGGATGACGAGAGGAGGGTGAGCATGAGGAGAGT 588
DB 572 ATGCTGAGGGCTACGTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGAGT 631
QY 589 ATGATCAAGATGCTCAGGTAGTGGAGAGATGAGGAGGCCGAGGAGGAGGAGGAGAGT 648
DB 632 ATGATCAAGATGCTCAGGTAGTGGAGAGATGAGGAGGCCGAGGAGGAGGAGGAGAGT 691
QY 649 AAGAGGAGGACCTGAGTGGAGGGGAGGAGGAGGATCAAGAGCTTATAACGATGAGAGG 708
DB 692 AAGAGGAGGACCTGAGTGGAGGGGAGGAGGAGGATCAAGAGCTTATAACGATGAGAGG 751
QY 709 TAGATGGCAGAGAGATGATGAAGAGAGCTTGGTGAAGAGAGAGAGGGGTGAGAGGCAAAAT 768
DB 752 TAGATGACGAGAGAGATGATGAAGAGAGCTTGGTGAAGAGAGAGAGGGGTGAGAGGCAAAAT 811
QY 769 GAGAACTGAAGATGAGGAGAGAGATGATGAAGTGAAGTAACTATTTTGAAGAAATTT 828
DB 812 GAGAACTGAAGATGAGGAGAGAGATGATGAAGTGAAGTAACTATTTTGAAGAAATTT 871
QY 829 CCTATTGATTTGACTGTTTTTACCCATATCCCTC-----CCCCCTCCCAATCCTGCC 882
DB 872 CCTATTGATTTGACTGTTTTTACCCATATCCCTC-----CCCCCTCCCAATCCTGCC 931
QY 883 CCCTGAA 889
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Db 932 CCCTGAA 938

RESULT 7

US-08-466-603-3
; Sequence 3, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: mus sp
; US-08-466-603-3

Query Match 64.2%; Score 570.8; DB 1; Length 980;

Best Local Similarity 82.9%; Pred. No. 5.4e-127;

Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;

QY 50 ACAGAGAGCGCAGAGATGGAGATGGCGACGACGGATTCATTTCAGAGCTCGGAGACAGGGC 109
DB 10 AGAGAGAGCGCAGAGATGGAGATGGACAAACGGATTTATTTCAGAGCTCGGAGACAGGAC 69
QY 110 GCCCTCTGATGTGAAGAACTTGCCTGGACACACAGTCGCTGAATGAAGGCAAACTCGA 169
DB 70 GCCCTCTGATGTGAAGAGCTTGGTCTGGATTAAGTCAATTCAGTCAATTCAGGCAAAATCGA 129
QY 170 AGCCCTCACAGATGAATTTGAAGAACTTGAAGTCTTAAAGTAAATCAACGAGGCGCTCAC 229
DB 130 AGGCTTCAGGGATCAGTTTGAAGAACTTGAAGTCTTAAAGTCAATTCAGTCAATTCAGGCAAAATCGA 189
QY 230 CTCATCTCAGACATTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 277
DB 190 CTCATCTCAGACATTACCAAGTTTAAACAACTCAAGAACTTGAATTAAGCGGAAACAG 249
QY 278 AGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCAGCATCTATATTT 337
DB 250 AATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACTTAAAGCATCTAAATTT 309

QY	338	AAGTGGCAACAAATTAAGAC	CCCTAGCACAAATAGAC	CCCACTGAACACAGTTTGA	AAACCT	397
Db	310	AAGTGGCAACAAATTAAGAT	CTCAGCACAAATAGAC	CCCTCAAGAACTTAGA	AAATCT	369
QY	398	CAGAGCTTAGACCTTTCAAT	TGCAGGTACCAACCTTG	ACGACTACGGAGAAA	ACGT	457
Db	370	CAAGAGCTTAGACCTGTTT	AACCTGAGGTGACCAAC	CTGAATGCTACCGAGA	AAACGT	429
QY	458	GTTCAAGCTTCTCCTGCA	ACTACATCTCGACAGCTG	TACTGGGACCAACAAG	GAGC	517
Db	430	GTTCAAGCTCCTGCCCA	GCTCATCTCGATGGCTT	ATGACAGGGACAACAG	GAGGC	489
QY	518	CCCTTACTCAGATATTGAG	CACCACCTGGAGGGCCT	TGGATGACGAGGAGGG	TGACGA	577
Db	490	CCCCGACTCCGATGTTG	AGGGCTACGTGGA-----	GGATGACGACGAGAG	ATGACGA	543
QY	578	TGAGGAGGATATGATGA	AGATGCTCAGGTAGTGG	AAAGATGAGGAGGGC	GAGGAGGA	637
Db	544	TGAGGAGGAGTATGATG	AATATCCACAGCTAGT	TGGAAGATGAAGAG	AAGAGGTTGACGA	603
QY	638	GGAGGAAGGTGAAGAG	GAGACGTGAGTGGAGGG	GACGAGGAGGTGAAG	AGGTTATAA	697
Db	604	GGAGAAGGGGAGGAAG	AGGATGTGAGTGGAG	AGGAGGAGGATGAG	GAAGGTTACAA	663
QY	698	CGATGGAGAGGTAGATG	CCAGGAAGTGNAG	AGAGCTTGGTGAAG	AGAAAAGGGGTCA	757
Db	664	TGACGGGAAGTGGATG	ACAGGAAGACGAAGA	AGAGCTGGTGAAGA	AGAAGGGAGTCA	723
QY	758	GAAGCGAAATGAGAC	CTCAAGATGAGGGAG	AAAGATGATGACTA	AGTAGAATAACCTAT	817
Db	724	GAAGCGAAACGAGAAC	CCGACGATGAGGC	GGAAGAGGATGACTA	AGGA-ATGAACCTGT	782
QY	818	TTTGAAAATTCCTATTG	TGATTGACTGTTTTT	TACCCATATCCCC	CTCCCCCTCCCAATC	877
Db	783	TTGGGGAATTCCTATTG	TGATTGACTGTTTTT	TACCCATATCCCC	CTCCCCCTCCCTATTC	842
QY	878	CTGCCCCCTGAA	889			
Db	843	CTGCCCCCGAA	854			

RESULT 8
US-08-314-503A-3
; Sequence 3, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5734022el. Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: mus sp
; US-08-314-503A-3

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Query Match		64.2%	Score 570.8;	DB 1;	Length 980;
Best Local Similarity		82.9%	Pred. No. 5.4e-127;		
Matches	706;	Conservative	0;	Mismatches 127;	Indels 19;
Gaps					
Qy	50	ACAGAGCGCGAGAGATGGACACAGCGATTCATTTCAGAGCTCGCGAACAGGC	109		
Db	10	AGAGAGCGCGAGAGATGGCAACACGGATTTATTTCAGCTCGGCACAGGAC	69		
Qy	110	GCCCTCTGATGTGAAGAACTTGCCTTGGCAACAGTCGGTCAATGAAGGCAAACTCGA	169		
Db	70	GCCCTCTGATGTGAAGAGCTGGTCTGGTAACTGTAAGTCAATTGAAGGCAAAATCGA	129		
Qy	170	AGCCCTCACAGATGAATTTGAAGAACTTGAATCTTTNAGTAAATCAACGAGGCGCTCAC	229		
Db	130	AGGCCTCACGATGAGTTTGAAGAACTTGAATCTTAAAGTACAATCAACGTAGGCGCTCAC	189		
Qy	230	CTCAATCTCAGACTTACCAAGTTA---AGTTTGAGNAAGCTTTGAACCTA-----AG	277		
Db	190	CTCATTTTCCAACCTTACCAAGTTTAAACAACCTCAAGAACTTGAATTAAGCGAAAAACAG	249		
Qy	278	AGTCTCAGGGGGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTTCACGCATCTATATTT	337		
Db	250	AATCTCAGGGGACCTGGAGTATTGGCAGAGAAATGTCCCAACCTTTAAGCATCTAAATTT	309		
Qy	338	AAGTGGCAACAAAATTAAGACACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAAACCT	397		
Db	310	AAGTGGCAACAAAATAAAGATCTCAGCACAAATAGAGCGCTGAAGAAGTTTAGAGAATCT	369		
Qy	398	CAAGAGCTTAGACCTTTTCAATTGCGAGGTTAACCAACCTGAACGACTACGGAGAAAAACGT	457		
Db	370	CAAGAGCCTAGACCTGTTTAACTGTGAGTGCACCAACCTGAAATGCCCTACCCGAGAAAAACGT	429		
Qy	458	GTTCAAGCTTCTCCTCGCAACTCACATATCTCGACAGCTGTTACTGGACACCACAGGAGGC	517		
Db	430	GTTCAAGCTTCTCGCCAGGTCATGTACCTCGATGGCTATGACAGGGACAAACAGGAGGC	489		
Qy	518	CCCTTACTTCAGATATTGAGGACCACAGTGGAGGGCTGGATGACGAGGAGGAGGCTGAGCA	577		
Db	490	CCCGACTCCGATGTTGAGGGCTACGTGGA-----GGATGACGACGAGGAAGATGAGGA	543		
Qy	578	TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGGCGGAGGAGGGA	637		
Db	544	TGAGGAGAGTATCATGAATATGCCAGCTAGTGGAAAGATGAAGAGGAAGAGGTTGAGGA	603		
Qy	638	GGAGGAGGTTGAAGAGAGGACGTGATGTGAGGGGGCAGGAGGATGAAGAAGGTTATAA	697		
Db	604	GGAGAAGGGGAGGAAGGAGTGTGAGTGGAGAGGAGGAGGAGGATGAGGAGGAAGGTTACAA	663		
Qy	698	CGATGGAGAGTACATGGCAGGAAGATGAAGAAGAGCTTTGGTGAAGAAGAAAGGGGTCA	757		
Db	664	TGACGGGAAGTGGATGACGAGGAGAGACGAAGAAGAAGCTGGTGAAGAAGAAGGGAGTCA	723		
Qy	758	GAAGCGAAAATGAACACTGAAGATGAGGGAGAGAAGATGATCACTTAAGTAGAATAAACCTAT	817		
Db	724	GAAGCGAAAACGAAACCGACGATGAGGGCGAAGAGATGACTTAAGGA-ATGAACCTGT	782		
Qy	818	TTTGAAAATTCCTATTGTGATTTGACTGTTTTTACCCATATCCCTCCCTCCCTCCCAATC	877		
Db	783	TTGGGGAATTCCTATTGTGATTTGACTGTTTTTACCCATATCCCTCCCTCCCTCCCTATTC	842		

QY 878 CTGCCCCCTGAA 889
Db 843 CTGCCCCCGAA 854

RESULT 9

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US-08-468-066-3
; Sequence 3, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: mus sp
US-08-468-066-3

Query Match 64.2%; Score 570.8; DB 1; Length 980;
Best Local Similarity 82.9%; Pred. No. 5.4e-127;
Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;

QY 50 ACAGAGAGCGGAGAGATGGAGATGGGAGACAGCGATTTCATTTCAGAGCTGCGGAACAGGGC 109
Db 10 AGAGAGAGCGGAGAGATGGAGATGGACAAACGGATTATTATTAGAGCTGCGGAACAGGAC 69

QY 110 GCCCTCTGATGGAAGAACTTGCCTCGGACACAGCTCGGTCGAAATGAAGGCAAACTCGA 169
Db 70 GCCCTCTGATGGAAGAACTTGCCTCGGATCACTGTAAGTCAATTAAGTCAATTAAGGCAAACTCGA 129

QY 170 AGCCCTCAGATGAATTTGAAGAACTGGAATTCCTTAGTAATAATCAACGAGGCGCTCAC 229
Db 130 AGCCCTCAGGATGAGTTGAAGAACTGGAATTCCTTAGTAATAATCAACGAGGCGCTCAC 189

QY 230 CTCATCTCAGACTTACCAAAAGTTA--AAGTTGAGAAAGCTTGAACCTA-----AG 277
Db 190 CTCATCTCAGACTTACCAAAAGTTA--AAGTTGAGAAAGCTTGAATTAAGCGAAACAG 249

QY 278 AGTCTCAGGGGCGCTGGGAAGTATTGGGAGAAAAGTGTCCAAAACCTCAGGCATCTATATTT 337
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Db 250 AATCTCAGGGGACCTGGAGTATTGGCAGAGAAATGTCCGAACCTTTAAGCATCTAAATTT 309
QY 338 AAGTGGCAACAAAATTAAAGACCTCAGCAACATAGAGCCACTGAAACAGTTAGAAAACCT 397
Db 310 AAGTGGCAACAAAATTAAAGATCTCAGCAACATAGAGCCCTGAAAGATTTAGAAATCT 369
QY 398 CAAGAGCTTAGACCTTTTCAATTTGCGAGGTAAACCACTGAACGACTACGGAGAAAACGT 457
Db 370 CAAGAGCTTAGACCTGTTTAACTGTGAGGTGACCACTGAATCCCTACCGAGAAAACGT 429
QY 458 GTTCAAGCTTCTCCTCGAACTCACATATCTCGACACCTGTTACTGGGACCAACAAGGAGGC 517
Db 430 GTTCAAGCTCTCCTCCCGAGGTCACTGACCTCGATGCTATGACAGGAGCAACAAGGAGGC 489
QY 518 CCCTTACTCAGATATTGAGGACCACTGGAGGCGCTGGATGAGGAGGAGGAGGTTGAGCA 577
Db 490 CCCCGACTCGGATGTTGAGGGCTACGTGGA-----GGATGAGCGAGGAGAGATGAGGA 543
QY 578 TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGA 637
Db 544 TGAGGAGGAGTATGATGAATATCCCGAGCTAGTGGAGATGAGGAGGAGGAGGTTGAGGA 603
QY 638 GGAGGAAGGTGAAGAGGAGGACCTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATAA 697
Db 604 GGAAGAAGGGGAGGAGAGGATGTGAGTGGAGAGGAGGAGGAGGATGAGGAAGGTTTACAA 663
QY 698 CGATGGAGAGGTAGATGGCGAGCAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCA 757
Db 664 TGACGGGGAAGTGGATGACGAGGAAGACGAAGAAGAGCTGGTGAAGAAGAAGGGAGTCA 723
QY 758 GAAGCGAAAATGAGAACTGGAAGATGAGGAGAGAGATGATGACTAAGTAGAATAACCTAT 817
Db 724 GAAGCGAAAACGAGAACCGGACGATGAGGCGAAGAGGATGACTAAGGA-ATGAACCTGT 782
QY 818 TTTGAAAATTCCTATTGTGATTTGACTGTGTTTACCCTATCCCTCCCTCCCTCCCAATC 877
Db 783 TTGGGGAATTCCTATTGTGATTTGACTGTGTTTACCCTATCCCTCCCTCCCTCCCTATTC 842
QY 878 CTGCCCCCTGAA 889
Db 843 CTGCCCCCGAA 854

RESULT 10
US-08-466-717-3
; Sequence 3, Application US/08466717
; Patent No. 5874234
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,717
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
```

ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: mus sp
US-08-466-717-3

Query Match 64.2%; Score 570.8; DB 2; Length 980;
Best Local Similarity 82.9%; Pred. No. 5.4e-127;
Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;

QY 50 ACAGAGAGCGGAGAGATGGAGATGGCGACACAGGATTCATTACAGAGCTGCGGAACAGGC 109
DB 10 AGAGAGAGCGGAGAGATGGAGATGGCAAAACGGATTTATTAGAGCTGCGGAACAGGC 69
QY 110 GCCCTCTGATGTGAAGAACTTGCCTGGACACAGTCGGTGGATGGAATGAAGGCAAACTCGA 169
DB 70 GCCCTCTGATGTGAAGAACTTGCCTGGATTAACCTGAATTAAGGCAAACTCGA 129
QY 170 AGCCCTCACAGATTAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGA 229
DB 130 AGCCCTCACAGATTAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGA 189
QY 230 CTCATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 277
DB 190 CTCATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 249
QY 278 AGTCACAGGGGCTGCAAGTATGGCAGAAAGTGTCCAAACCTCAGCATCTATATTT 337
DB 250 AATCTCAGGGGCTGCAAGTATGGCAGAAAGTGTCCAAACCTCAGCATCTATATTT 309
QY 338 AAGTGGCAACAAATTAAGAACCTCAGCAATAGAGCCACTGAAACAGTTAGAAACCT 397
DB 310 AAGTGGCAACAAATTAAGAACCTCAGCAATAGAGCCACTGAAACAGTTAGAAACCT 369
QY 398 CAAGAGCTTAGACCTTTCAATTCGAGGTAAACCACTGAAGCTACGAGGAAACGT 457
DB 370 CAAGAGCTTAGACCTTTCAATTCGAGGTAAACCACTGAAGCTACGAGGAAACGT 429
QY 458 GTTCAAGCTTCTCTGCAACTCACAATATCTCGACAGCTGTACTGGGACCAAGAGGC 517
DB 430 GTTCAAGCTTCTCTGCAACTCACAATATCTCGACAGCTGTACTGGGACCAAGAGGC 489
QY 518 CCCTTACTCAGATATTAGGACCACTGAGGAGGCTGGATGACGAGGAGGAGGTGAGCA 577
DB 490 CCCGACTCCGATGTTAGGGCTACGTGGA-----GGATGACGAGGAGGAGGTGAGCA 543
QY 578 TGAGGAGGATGATGAAATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGA 637
DB 544 TGAGGAGGATGATGAAATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGA 603
QY 638 GGAGGAAGGTGAAGAGGAGGAGGAGTGTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 697
DB 604 GGAGGAAGGTGAAGAGGAGGAGGAGTGTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663
QY 698 CGATGGAGAGGTAGATGGCAGGAGGAGTGAAGAGAGCTTGGTGAAGAGGAGGAGGAGG 757
DB 664 TGACGGGGAAGTGTGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTCA 723
QY 758 GAACCGAAATGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 817
DB 724 GAACCGAAATGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 782

QY 818 TTGAAAAATTCCTATTGTGATTGACTGTTTTTACCCTATATCCCTCCCTCCCTCAATC 877
DB 783 TTGGGAAATTCCTATTGTGATTGACTGTTTTTACCCTATATCCCTCCCTCCCTCAATC 842
QY 878 CTGCCCCCTGAA 889
DB 843 CTGCCCCCTGAA 854

RESULT 11
US-08-466-743-3
Sequence 3, Application US/08466743
Patent No. 6040173
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,743
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/314,503
APPLICATION NUMBER: US/08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: mus sp
US-08-466-743-3

Query Match 64.2%; Score 570.8; DB 3; Length 980;
Best Local Similarity 82.9%; Pred. No. 5.4e-127;
Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;

QY 50 ACAGAGAGCGGAGAGATGGAGATGGCGACACAGGATTCATTACAGAGCTGCGGAACAGGC 109
DB 10 AGAGAGAGCGGAGAGATGGAGATGGCAAAACGGATTTATTAGAGCTGCGGAACAGGC 69
QY 110 GCCCTCTGATGTGAAGAACTTGCCTGGACACAGTCGGTGGATGGAATGAAGGCAAACTCGA 169
DB 70 GCCCTCTGATGTGAAGAACTTGCCTGGATTAACCTGAATTAAGGCAAACTCGA 129
QY 170 AGCCCTCACAGATTAAGTGAAGAACTTGAAGAACTTGAAGTAAATCAACGGAGGCTCAC 229
DB 130 AGCCCTCACAGATTAAGTGAAGAACTTGAAGAACTTGAAGTAAATCAACGGAGGCTCAC 189

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QY 230 CTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 277
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Db 190 CTCCATTTCCAACCTTACCAAAAGTTAACAACAACTCAAGAAAGCTTGAATTAAGCGAAACAG 249
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 278 AGTCTCAGGGGCCCTGGAGTAGTATGGCAGAAAAGTGTCCAAACCTCAGGCATCTATATTT 337
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 AATCTCAGGGGACCTGGAGTAGTATGGCAGAAAAGTGTCCGAACTTAAAGCATCTAAATTT 309
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 338 AAGTGGCAACAAAATTAAGAGCTTCAGCACAAATAGAGCCACTGAAACAGTTTAGAAAACCT 397
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 AAGTGGCAACAAAATTAAGAGCTTCAGCACAAATAGAGCCCGTGRAGAAGTTAGAGATCT 369
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 CAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGGAGAAAACGT 457
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 370 CAAGAGCTTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCCCTACCGAGAAAACGT 429
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 458 GTTCAAGCTTCTCCTGCAACTCACAATCTCAGACAGCTGTTACTGGGACCACAGAGGC 517
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 GTTCAAGCTTCTCCTGCAACTCACAATCTCAGACAGCTGTTACTGGGACCACAGAGGC 489
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 518 CCCTTACTCAGATATTGAGGACCACAGCTGGAGGCGCTGGATGACGAGGAGGCTGAGCA 577
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 490 CCCCGACTCCGATGTTGAGGCGCTACGTGGA-----GGATGACGACGAGGAAGATGAGGA 543
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 578 TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGA 637
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 TGAGGAGGAGTATGATGAATGATGCCAGCTAGTGTGAAGATGAAGAGGAAAGGTTGAGGA 603
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 638 GGAGGAGGAGTGAACGAGGAGGACGTGAGTGAGGGGACGAGGAGGATGAACAAAGTTATAA 697
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 604 GGAAGAGGGGAGGAGGAGGATGTGAGTGGAGAGGAGGAGGAGGATGAGGAAGGTTACAA 663
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 698 CGATGGAGAGGTAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAAGAGGGGTCA 757
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 664 TGACGGGGAAGTGGATGACGAGAGAGACGAGAAAGCTGGTGAAGAAAGAGGAGTCA 723
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 758 GAAGCGAAAATGAGAACCTTGAAAGATGAGGGAGAAAGATGATGACTAAGTAGAATAACCTAT 817
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 GAAGCGAAAATGAGAACCTTGAAAGATGAGGGAGAAAGATGATGACTAAGTAGAATAACCTAT 782
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 818 TTTGAAAATTCCTATTGTGATTTGACTGTTTACCATATCCCTCCCGCTCCCAATC 877
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 783 TTTGAAAATTCCTATTGTGATTTGACTGTTTACCATATCCCTCCCGCTCCCAATC 842
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 878 CTGCCCCCTGAA 889
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 843 CTGCCCCCGGAA 854
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 12
PCT-US95-12414-3
; Sequence 3, Application PC/TUS9512414
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: Novel Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12414
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoscheit Esq., Dale H.
; REGISTRATION NUMBER: 19,090
; REFERENCE/DOCKET NUMBER: 1107.51507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: mus sp
; PCT-US95-12414-3
```

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Query Match 64.2%; Score 570.8; DB 5; Length 980;
Best Local Similarity 82.9%; Pred.No.5.4e-127;
Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;

QY 50 ACAGAGAGCGGAGAGATGGAGATGGGACGCGATTCATTTCAGAGCTGCGGAACAGGCG 109
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10 AGAGAGAGCGGAGAGATGGAGATGGGACGCGATTCATTTCAGAGCTGCGGAACAGGCG 69
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 110 GCCCTCTGATGTGAAGAAGCTTGCCTGGACACAGCTCGGTGCGAANTGAAGGCAAACTCGA 169
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 GCCCTCTGATGTGAAGAAGCTTGCCTGGATAACTGTAACTCAATTGAAGGCAAAATCGA 129
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 AGCCTCACAGATGAATTTGAAGAAGCTTGAAGTAACTCAAGTAACTCAAGTAACTCAAG 229
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 AGGCTCACGAGTGAATTTGAAGAAGCTTGAAGTAACTCAAGTAACTCAAGTAACTCAAG 189
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 CTCATCTCAGACTTACCAAGTTA---AAGTTGAGAAAAGCTTGAACCTA-----AG 277
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 CTCATTTCCAACCTTACCAAGTTA---AAGTTGAGAAAAGCTTGAACCTA-----AG 249
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 278 AGTCTCAGGGGCGCTGGAAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTT 337
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 AATCTCAGGGGCGCTGGAAGTATTTGGCAGAAAAGTGTCCAAACCTTAAAGCATCTAAATTT 309
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 338 AAGTGGCAACAAAATTAAGAGCTTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCT 397
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 AAGTGGCAACAAAATTAAGAGCTTCAGCACAAATAGAGCCCGTGRAGAAGTTAGAGATCT 369
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 CAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGGAGAAAACGT 457
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 370 CAAGAGCTTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCCCTACCGAGAAAACGT 429
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 458 GTTCAAGCTTCTCCTGCAACTCACAATCTCAGACAGCTGTTACTGGGACCACAGAGGC 517
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 GTTCAAGCTTCTCCTGCAACTCACAATCTCAGACAGCTGTTACTGGGACCACAGAGGC 489
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 518 CCCTTACTCAGATATTGAGGACCACAGCTGGAGGCGCTGGATGACGAGGAGGCTGAGCA 577
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 490 CCCCGACTCCGATGTTGAGGCGCTACGTGGA-----GGATGACGACGAGGAAGATGAGGA 543
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 578 TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGA 637
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 TGAGGAGGAGTATGATGAATGATGCCAGCTAGTGTGAAGATGAAGAGGAAAGGTTGAGGA 603
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 638 GGAGGAGGAGTGAACGAGGAGGACGTGAGTGAGGGGACGAGGAGGATGAACAAAGTTATAA 697
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 604 GGAAGAGGGGAGGAGGAGGATGTGAGTGGAGAGGAGGAGGAGGATGAGGAAGGTTACAA 663
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 698 CGATGGAGAGGTAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAAGAGGGGTCA 757
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 664 TGACGGGGAAGTGGATGACGAGAGAGACGAGAAAGCTGGTGAAGAAAGAGGAGTCA 723
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 758 GAAGCGAAAATGAGAACCTTGAAAGATGAGGGAGAAAGATGATGACTAAGTAGAATAACCTAT 817
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 GAAGCGAAAATGAGAACCTTGAAAGATGAGGGAGAAAGATGATGACTAAGTAGAATAACCTAT 782
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 818 TTTGAAAATTCCTATTGTGATTTGACTGTTTACCATATCCCTCCCGCTCCCAATC 877
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 783 TTTGAAAATTCCTATTGTGATTTGACTGTTTACCATATCCCTCCCGCTCCCAATC 842
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 878 CTGCCCCCTGAA 889
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 843 CTGCCCCCGGAA 854
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db	84	CTAAATTTAAGTGCACAAAATAAAAGATCTCAGCACAAATAGACGCGCTGAAGAAGCTTA	143
Qy	350	GAAAACCTCAAGAGCTTAGACCTTTTCAATTCGCAGGTAAACCACTGAACGACTACGGA	449
Db	144	GAGAACTTCAAGAGCCCTAGACCTTTTAACTGTGAGGTGACCAACCTGAATGCTTACCGA	203
Qy	450	GAAAACGTGTTCAAGCTTCTCCTCAACTCACATATCTGCACAGCTCTTACTGGGACCAC	509
Db	204	GAAAACGTGTTCAAGCTCCTGCCCCAGGTCATGTACCTCGATGGCTATGACAGGGACAAC	263
Qy	510	AAGGAGGCCCTTACTCAGATATTGAGGACCAAGTGGAGGGCCTGGATGACGAGGAGGAG	569
Db	264	AAGGAGGCCCCCGACTCCGATGTTGAGGGCTAAGTGA-----GGATGACGACGAGGAA	317
Qy	570	GCTCAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTACTGGAAGATGAGGAGGGCGAG	629
Db	318	GATCAGGATGAGGAGGAGTATGATGAATATGCCACGCTACTGGAAGATGAAGAGGAAGAG	377
Qy	630	CAGGAGGAGGAGGAAGGTGAAGAGGAGGACCTGAGTGGAGGGACGAGGAGGATGAAGAA	689
Db	378	GTTCAGGAGGAAGAAGGGAGGAGAGGATGTGATGGCAGAGGAGGAGGATGAGGAA	437
Qy	690	GTTTATTAACGATGAGAGGTAGATGGCGAGAGATGAAGAAGCTTGGTGAAGAAGAA	749
Db	438	GTTTACAATCAGCGGGGAAGTGGATGACGAGGAAGACGAAGAAGAAGCTGTTGAAGAAGAA	497
Qy	750	AGGGGTGAGAGGCGAAATCAGAACCTGAAGATCAGGAGGAAGTATGATGACTAAGTAGAA	809
Db	498	GGGAGTCAGAAAGCGAAACAGAAACCGGACGATGAGGGCGAAGAGATGACTAAGGA-AT	556
Qy	810	TAACCTATTTTGAATAATTCCTATTTGTGATTGACTGTTTTTACCCTATATCCCTCCCCC	869
Db	557	GAACCTGTTGGGAAATTCCTATGTGATTGACTGTTTTTACCCTATATCCCTCCCCC	616
Qy	870	CTCCAATCTGCCCCCTGAA	889
Db	617	TCCTATTCCCTGCCCCCGAA	636

RESULT 13

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QY 570 GGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGAG 6239
DB 318 GATGAGGTGAGGAGGAGTATGATGAATATGCCAGCTACTGGAAGATGAAGAGGAAGAG 377
QY 630 GAGGAGGAGGAGGAAGTGAAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAA 689
DB 378 GTTGAGGAGGAAGAAGGGGAGGAGGAGGATGTGAGTGGAGGAGGAGGAGGATGAGGAA 437
QY 690 GGTTTATACGATGAGAGGTAGTGGCGAGGAAGATGAAGAAAGAGCTTGCTGAAGAAGAA 749
DB 438 GTTTACATGACGGGGAAGTGGATGACGAGGAAGACGAAGAAGAGCTGGTGAAGAAGAA 497
QY 750 AGGGGTGAGAGCGAAATGAGAACCTGAAGATGAGGGAGGAAGATGATGACTAAGTAGAA 809
DB 498 GGGAGTCAGAAGCGAAACAGAACCGGACGATGAGGGCGAAGAGGATGACTAAGGA-AT 556
QY 810 TAACCTATTTTGAAGAAATTCCTATTGTGATTGACTGTTTTTACCCTATCCCCCTCCCC 869
DB 557 GAACCTGTTGGGAAATTCCTATTGTGATTGACTGTTTTTACCCTATCCCCCTCCCC 616
QY 870 CTCCAATCCTGCCCCCTGAA 889
DB 617 TCCTATTCTGCCCCCGAA 636

RESULT 14
US-08-314-503A-4
; Sequence 4, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5734022zel Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299

```

APPLICATION NUMBER: US/08/314,503A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299

```

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-314-503A-4

Query Match 48.3%; Score 429.2; DB 1; Length 759;
Best Local Similarity 83.1%; Pred. No. 2.4e-93;
Matches 515; Conservative 0; Mismatches 98; Indels 7; Gaps 2;

QY 270 GAACCTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCAT 329
DB 24 GAAACAGAAATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCAT 83
QY 330 CTATATTTAAGTGGCAACAATAATTAAAGACCTCAGACCAATAGAGCCACTGAAACAGTTA 389
DB 84 CTAATTTAAGTGGCAACAATAATAAAGATCTCAGACCAATAGAGCCGCTGAAGAAGTTA 143
QY 390 GAAACCTCAGAGCTTAGACCTTTCAATTGCGAGGTAACCAACCTGAACGACTACGGA 449
DB 144 GAGATCTCAGAGCCCTAGACCTGTTAACTGTGAGGTGACCAACCTGAATGCTTACCGA 203
QY 450 GAAACCTGTTTAAAGCTTCTCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAC 509
DB 204 GAAACCTGTTTAAAGCTTCTCCTGCCCGGCTGATGATGATGATGATGATGATGATGATGAT 263
QY 510 AAGAGGCCCTTACTCAGATATTAGGAGCCACGTGGAGGGCCCTGGATGACGAGGAGGAG 569
DB 264 AAGAGGCCCTTACTCAGATATTAGGAGCCACGTGGAGGGCCCTGGATGATGATGATGATGAT 317
QY 570 GGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGTGTGGAAGATGAGGAGGCGGAG 629
DB 318 GATGAGCATGAGGAGGAGTATGATGAATATGATGATGATGATGATGATGATGATGATGATGAT 377
QY 630 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 378 GTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
QY 690 GGTATTAACGATGAGAGGTAGATGCCAGGAGAGATGAAGAGAGCTTGGTGAAGAAGAA 749
DB 438 GGTATTAACGATGAGAGGTAGATGCCAGGAGAGATGAAGAGAGCTTGGTGAAGAAGAA 497
QY 750 AGGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 809
DB 498 GGGAGTCAAGACGAAACGAGAGACCGACGATGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 556
QY 810 TAACCTATTTTGAATAATTCCTATTGTGATTTGATGCTGTTTAACTGATGCTGTTTAACTG 869
DB 557 GAACTGTTTGGGAAATTCCTATTGTGATTTGATGCTGTTTAACTGATGCTGTTTAACTGAT 616
QY 870 CTCCATCTGCCCCCTGNA 889
DB 617 TCCTATTCTGCCCCCGAA 636

RESULT 15
US-08-468-066-4
; Sequence 4, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhaida, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-468-066-4

Query Match 48.3%; Score 429.2; DB 1; Length 759;
Best Local Similarity 83.1%; Pred. No. 2.4e-93;
Matches 515; Conservative 0; Mismatches 98; Indels 7; Gaps 2;

QY 270 GAACCTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCAT 329
DB 24 GAAACAGAAATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCAT 83
QY 330 CTATATTTAAGTGGCAACAATAATTAAAGACCTCAGACCAATAGAGCCACTGAAACAGTTA 389
DB 84 CTAATTTAAGTGGCAACAATAATAAAGATCTCAGACCAATAGAGCCGCTGAAGAAGTTA 143
QY 390 GAAACCTCAGAGCTTAGACCTTTCAATTGCGAGGTAACCAACCTGAACGACTACGGA 449
DB 144 GAGATCTCAGAGCCCTAGACCTGTTAACTGTGAGGTGACCAACCTGAATGCTTACCGA 203
QY 450 GAAACCTGTTTAAAGCTTCTCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAC 509
DB 204 GAAACCTGTTTAAAGCTTCTCCTGCCCGGCTGATGATGATGATGATGATGATGATGATGAT 263
QY 510 AAGAGGCCCTTACTCAGATATTAGGAGCCACGTGGAGGGCCCTGGATGACGAGGAGGAG 569
DB 264 AAGAGGCCCTTACTCAGATATTAGGAGCCACGTGGAGGGCCCTGGATGATGATGATGATGAT 317
QY 570 GGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGTGTGGAAGATGAGGAGGCGGAG 629
DB 318 GATGAGCATGAGGAGGAGTATGATGAATATGATGATGATGATGATGATGATGATGATGATGAT 377
QY 630 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 378 GTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
QY 690 GGTATTAACGATGAGAGGTAGATGCCAGGAGAGATGAAGAGAGCTTGGTGAAGAAGAA 749
DB 438 GGTATTAACGATGAGAGGTAGATGCCAGGAGAGATGAAGAGAGCTTGGTGAAGAAGAA 497
QY 750 AGGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 809
DB 498 GGGAGTCAAGACGAAACGAGAGACCGACGATGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 556
QY 810 TAACCTATTTTGAATAATTCCTATTGTGATTTGATGCTGTTTAACTGATGCTGTTTAACTG 869
DB 557 GAACTGTTTGGGAAATTCCTATTGTGATTTGATGCTGTTTAACTGATGCTGTTTAACTGAT 616
QY 870 CTCCATCTGCCCCCTGNA 889
DB 617 TCCTATTCTGCCCCCGAA 636
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 22:43:58 : Search time 40.5891 Seconds
(without alignments)
8540.478 Million cell updates/sec

Title: US-09-591-500-3
Perfect score: 889
Sequence: 1 ggggtcagggtttattgatt.....ctccaatcctgccccctgaa 889

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175.4	19.7	718	10	US-09-910-943-76
2	171.8	19.3	771	10	US-09-910-943-166
3	171.6	19.3	748	10	US-09-910-943-132
4	146	16.4	763	10	US-09-910-943-622
5	127.6	14.4	557	9	US-10-046-935-2145
6	127.6	14.4	557	9	US-09-878-178-2145
7	121.2	13.6	720	9	US-10-101-487-74
8	121.2	13.6	720	9	US-10-101-487-76
9	118.6	13.3	522	9	US-10-101-487-71
10	118.6	13.3	530	9	US-10-101-487-73
11	118.6	13.3	554	9	US-10-101-487-69
12	118.6	13.3	554	9	US-10-101-487-106
13	102.8	11.6	575	10	US-09-864-761-20733
14	102.8	11.6	1969	10	US-09-864-761-3972
15	101	11.4	659158	9	US-09-771-208-20
16	94.4	10.6	423	10	US-09-864-761-18355
17	94.4	10.6	487	10	US-09-864-761-1597
18	92.6	10.4	344	10	US-09-864-761-19694
19	89.4	10.1	5387	9	US-10-001-873-22

c 20	89.2	10.0	53226	10	US-09-818-264-3	Sequence 3, Appl1
c 21	88.4	9.9	267	10	US-09-864-761-27984	Sequence 27984, A
c 22	88.4	9.9	474	10	US-09-864-761-11284	Sequence 11284, A
c 23	88.4	9.9	1944	10	US-09-864-761-2825	Sequence 2825, Ap
24	87.8	9.9	700	10	US-09-864-761-17529	Sequence 17529, A
25	87.6	9.9	3809	12	US-10-001-870-68	Sequence 68, Appl
c 26	84.2	9.5	399	10	US-09-864-761-2913	Sequence 2913, Ap
c 27	83.8	9.4	381	10	US-09-777-564-700	Sequence 700, App
28	83.6	9.4	390	10	US-09-790-399-7	Sequence 7, Appl1
29	83.4	9.4	299	10	US-09-864-761-21553	Sequence 21553, A
c 30	81.4	9.2	766	10	US-09-864-761-19608	Sequence 19608, A
c 31	80.8	9.1	438	10	US-09-864-761-4988	Sequence 4988, Ap
c 32	80.8	9.1	1282	9	US-10-002-344A-89	Sequence 89, Appl
c 33	80.6	9.1	305	10	US-09-864-761-19262	Sequence 19262, A
c 34	80.6	9.1	496	10	US-09-864-761-2534	Sequence 2534, Ap
35	80.2	9.0	4316	10	US-09-880-107-3713	Sequence 3713, Ap
36	80	9.0	350	10	US-09-822-263-19	Sequence 19, Appl
37	78.4	8.8	251	10	US-09-864-761-19674	Sequence 19674, A
38	78.4	8.8	345	10	US-09-822-263-17	Sequence 17, Appl
39	78.4	8.8	490	10	US-09-880-107-2261	Sequence 2261, Ap
40	78.4	8.8	497	10	US-09-822-263-33	Sequence 33, Appl
41	78.4	8.8	583	10	US-09-864-761-20772	Sequence 20772, A
42	78.4	8.8	1147	10	US-09-880-107-2311	Sequence 2311, Ap
43	78.4	8.8	1959	10	US-09-864-761-4012	Sequence 4012, Ap
c 44	77.4	8.7	276	10	US-09-864-761-20595	Sequence 20595, A
c 45	77.2	8.7	559	10	US-09-864-761-7684	Sequence 7684, Ap

ALIGNMENTS

RESULT 1

US-09-910-943-76
; Sequence 76, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/IG148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(718)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-76

Query Match	19.7%	Score 175.4;	DB 10;	Length 718;
Best Local Similarity	59.9%;	Pred. No. 1.8e-32;		
Matches 353;	Conservative 0;	Mismatches 221;	Indels 15;	Gaps 3;
Qy 64	AGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGGGAACAGGGCCCTCTGTATGTGA	123		
Db 132	ACATGGACATGAAAGAGATTGCTGGAGCTCAGGAATCGGNAAGCGGCTGACGCTA	191		
Qy 124	AAGAATTTCCTGGCAACACAGTCGGTCGAATGAAGCAAACTCGAAGCCCTACAGATG	183		
Db 192	AAGAATTGGTTCTAGATAACTGCCGTTTCAGACGATGGCAAAATTTATTGGACTGACCTCAG	251		
Qy 184	ATTTCGAGAAGCTGGAATTCCTTAAGTAAATCAACGGAGGCGCTACCTCAATCTCAGACT	243		
Db 252	AGTTTGAAGCTGGAGTTTCTCAGCATGATAAAATGTCAACTTATTTCTGTAGCTAACT	311		
Qy 244	TACCAAAAGTT---AAAGTTGAGAAAGCTTGAACATAA-----GAGTCTCAGGGGCC	291		
Db 312	TCCCAAGCTCCCAAGTTGAAAAAGCTGGAACTCAGTCAATCGAATCTCTGGAGGAT	371		

Query Match	16.4%;	Score 146;	DB 10;	Length 763;
Best Local Similarity	58.3%;	Pred. No. 1.6e-25;		
Matches 331;	Conservative 0;	Mismatches 221;	Indels 16;	Gaps
QY	64	AGATGAGATGGCGACACGGATTTCATTCAGACCTCGGGAAACAGGGCGCCTCTGATGTGA	123	
Db	134	ACATGGACATGAAAAGAGATTGATGCTGGAGCTCAGGAATCGGAAGCGGTGACGCTA	193	
QY	124	AGAACCTGCCCTGGCAACACAGTCGGTGCATTAAGGCAAACTCGAAGCCCTCACAGATG	183	
Db	194	AGAATTTGTTCTAGATACTGCCGTTACAGACGATGGCAAAATTAATGGACTGACCTCAG	253	
QY	184	AATTTGAAGAACTGGAAATCTTTAACTAAATCAACGGAGCGCTCACTCAATCTCAGACT	243	
Db	254	AGTTTGAAGCCTGGGATTTCTCAGCATGATAAATGTCAACTTAATATCTGTAGCTAACT	313	
QY	244	TACCAAAAGTT---AAAGTTGAGAAAGCTTGAACCTA-----GAGTCTCAGGGGGCC	291	
Db	314	TGCAAAAGCTCCCCAGTTTGA AAAAGCTGGAACCTCAGTGACAAATCGAATCTCTGCGAGAT	373	
QY	292	TGGAAGTATTGCGAGAAAAGTGTCAAAACCTCACGCATCTATATTAAAGTGCCACAAA	351	
Db	374	TAGAGTACTGGCAGAACGGACCCCAATTTGACACACCTGAACCTCAGTGGGAACAAGA	433	
QY	352	TTAAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGACTTTAGACC	411	
Db	434	TAAAAGAGATAAATACCTTAGAGCCACTTAAGAACTACCTCATCTCATGAGCTGAGCC	493	
QY	412	TTTTCAATTTGGGAGGTAACCAACCTGAACGACTACGGGAAAAACGTTTCAAGCTTCTCC	471	

Query Match	14.4%;	Score 127.6;	DB 9;	Length 557;
Best Local Similarity	56.0%;	Pred. No. 3.2e-21;		
Matches 241;	Conservative 0;	Mismatches 189;	Indels 0;	Gaps
QY	366	ACAAATAGAGCCACTGAACACAGTTAGAAAAACCTCAAGAGCTTTAGACCTTTTCAATTCGCGAG	425	
Db	1	ACAGTAGAAGCTCTGCAAAATCTTAAAAATTTGAAAGTCTTGACCTGTTAACTGTGAG	60	
QY	426	GTAACCAACCTGAACGACTACGGAGAAACGCTTCAAGCTTCTCTGCAACCTACACATAT	485	
QY	61	ATCAACAACCTGGAAGATTATAGAGAAAGTATTTTGAACACTACTGCGAGCAAACTACATAC	120	
QY	486	CTCGACAGCTTTACTGGGACCACAGGAGGCCCTTACTACATATTGAGGACCACGCTG	545	
Db	121	TTAGATCGAATTTGATCAGGAGGATATGAACCCCGGACTCTGAAGAGGAGGATGATGAG	180	
QY	546	GAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATGCTCAG	605	
Db	181	GATGCCATGAAGATGATGAAGAGGAGAGGAAATGAAGCTGGTCCACCGGAAGGATAT	240	
QY	606	GTACTGGAAGATGAGGAGCGGAGGAGGAGGAGAAAGTTCGAGGAGGAGGACCTCAGT	665	
Db	241	GAGGAGAGGAGGAGGAAGAGAGAGAGGAGATGAGGATGAGGATGAAGATGAAGATGAA	300	
QY	666	GGAGGGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGGTAGATGGCGAGGAGAT	725	
Db	301	GCAGGTTTCAGAGTTGGGAGAGGGAAGAGAGAAAGTGSGCCCTCTCATCTTAAATGAAAGAA	360	
QY	726	GAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAACCGAATAATGAGAACCTGGAAGTGA	785	
Db	361	GAATTCAGGATGAAGAAGATGATGACTATGTTGAAGAGGGGAAGAAGAGGAAGAA	420	
QY	786	GGAGAAGATG	795	
Db	421	GAGGAAGAAG	430	

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RESULT 6
US-09-878-178-2145
; Sequence 2145, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiaog, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878.178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2145
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-2145

Query Match      14.4%; Score 127.6; DB 9; Length 557;
Best Local Similarity 56.0%; Pred. No. 3.2e-21;
Matches 241; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 366 ACAATAGACCCACTGAACAGCTTAGAAAACCTCAAGACCTTAGACCTTTTCAATTCGCAG 425
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Db 1 ACAGTAGAAGCTCTCCAAANTCTTAAATAATTGAAAAGCTTTGACCTGTTTAACTGTGC 60

QY 426 GTAACCAACCTGAACGACTACGAGAAAACCTGTTCAAGCTTCTCCCTCAACTCACATAT 485
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ATCACAACCTGGAAGATTATAGAAAAGTATTTTGAACCTACTGCAGCAATCACATAC 120

QY 486 CTCAGACGCTGTACTGGGACCAACAGGAGGCCCTTACTCAGATATTAGGACCCACGTG 545
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TTAGATGGATTTCAGGAGGATAATCAAGCGCGGACTCTGAAGAGGAGGATGATGAG 180

QY 546 GAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATGCTCAG 605
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GATGCGATGAAGATGATCAAGAGGAAGAGGAAAATGAAGCTGTCCACCGGAAGGATAT 240

QY 606 GTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGT 665
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGAAGATGAGGATGAAGATGAAGAA 300

QY 666 GGAGGGGACGAGGAGGATGAAGAAGTTTATAACGATGAGGAGGATGATGCGGAGGAAGAT 725
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GCAGGTTACAGATTGGGAGAGGAGGAGGAGGAGGAGTGGGCCCTCTCATACTTAATGAAAGAA 360

QY 726 GAAGAAGAGCTTGGTGAAGAAGAAGGGGTCAGAAGCGAAAATGAGAACCTTGAAGATGAG 785
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Db 361 GAAATTCAGGATGAAGAAGATGATGATGACTATGTTGAAGAAGGGGGAAGAAGAGGAAGA 420

QY 786 GGAGAAGATG 795
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Db 421 GAGGAAGAAG 430

RESULT 7
US-10-101-487-74
; Sequence 74, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(718)
US-10-101-487-74

Query Match      13.6%; Score 121.2; DB 9; Length 720;
Best Local Similarity 61.9%; Pred. No. 1.1e-19;
Matches 192; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 503 GGACCACAAGGAGGCCCCCTTACTCAGATATTGAGGACCACGTGGAGGGCCTTGATGACGA 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 GGAAGAGGAGGAAGAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 414

QY 563 GGAGGAGGCTGACCATGACGAGGAGGAGCTATGATGAAGATGCTCAGGTAGTGSAGATGAGGA 622
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Db 415 AGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 474

QY 623 GCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 682
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Db 475 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 534

QY 683 TGAAGAAGGTTTATAACGATGAGAGGTTAGATGCCGAGGAGATGAAGAAGAGAGCTTGGTGA 742
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 594

QY 743 AGAAGAAGGGGTCAGAAAGCGAAATGAGAACCTTGAAGATGAGGAGGAGGAGGAGGAGGAGCA 802
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 654

QY 803 AGTAGAATAA 812
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Db 655 AGAGGAGGAA 664
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FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
LENGTH: 720
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(718)
US-10-101-487-74

Query Match      13.6%; Score 121.2; DB 9; Length 720;
Best Local Similarity 61.9%; Pred. No. 1.1e-19;
Matches 192; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 503 GGACCACAAGGAGGCCCCCTTACTCAGATATTGAGGACCACGTGGAGGGCCTTGATGACGA 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 GGAAGAGGAGGAAGAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 414

QY 563 GGAGGAGGCTGACCATGACGAGGAGGAGCTATGATGAAGATGCTCAGGTAGTGSAGATGAGGA 622
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 415 AGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 474

QY 623 GCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 682
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 475 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 534

QY 683 TGAAGAAGGTTTATAACGATGAGAGGTTAGATGCCGAGGAGATGAAGAAGAGAGCTTGGTGA 742
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Db 535 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 594

QY 743 AGAAGAAGGGGTCAGAAAGCGAAATGAGAACCTTGAAGATGAGGAGGAGGAGGAGGAGGAGCA 802
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Db 595 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 654

QY 803 AGTAGAATAA 812
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Db 655 AGAGGAGGAA 664

RESULT 8
US-10-101-487-76/c
; Sequence 76, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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[illegible]

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(without alignments)
11013.667 Million cell updates/sec

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Perfect score: 889
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Scoring table: IDENTITY_NUC

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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

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9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	729.8	82.1	894	9	AL533191
2	726.2	81.7	923	9	AL560249
3	724.2	81.5	875	9	AL535686
4	723.2	81.3	1034	9	AL518839
5	709.4	79.8	870	9	AL537874
6	705.8	79.4	875	9	AL547157

7	705.4	79.3	903	9	AL540827
8	693.6	78.0	992	9	AL517375
9	688	77.4	1035	14	BM904155
10	683.8	76.9	855	9	AL543743
11	668.6	75.2	853	9	AL535863
12	665.6	74.9	834	9	AL545880
13	661	74.4	895	14	BQ232856
14	659.6	74.2	1066	13	BM543218
15	645.2	72.6	894	9	AL571434
16	642.4	72.3	802	9	AL518247
17	627.2	70.6	999	13	BM460209
18	627	70.5	806	9	AL547462
19	620	69.7	749	13	BI860951
20	617	69.4	775	12	BF969229
21	612	68.8	961	13	BM475803
22	610.8	68.7	882	14	BQ427516
23	609.8	68.6	866	14	BQ687251
24	605.4	68.1	750	12	BG325466
25	600.2	67.5	902	9	AL516007
26	596.4	67.1	899	14	BQ890554
27	588.4	66.2	859	14	BQ212622
28	584	65.7	1141	11	AK020753
29	582.6	65.5	764	12	BG392351
30	581.6	65.4	1004	13	BM469555
31	566	63.7	737	9	AU122593
32	561.6	63.2	988	14	BQ216493
33	558.4	62.8	850	14	BQ229967
34	558.2	62.8	710	9	AL557479
35	555.2	62.5	764	10	BE561138
36	554.6	62.4	697	9	AU123726
37	551.8	62.1	683	10	BE544189
38	550.4	61.9	892	13	BI254991
39	547.6	61.6	790	10	BE409600
40	544.8	61.3	652	9	AL535685
41	541.4	60.9	762	10	BE561131
42	541.2	60.9	657	12	BF343748
43	533.2	60.0	728	9	AU130628
44	529.2	59.5	735	13	BI226535
45	528.8	59.5	742	12	BG287644

ALIGNMENTS

RESULT 1	AL533191	AL533191	894 bp	mRNA	linear	EST 13-FEB-2001
LOCUS	AL533191	LT1_FL015_Brn1	Homo sapiens	CDNA clone	CS0DN003YK10 5	
DEFINITION	AL533191	prime, mRNA sequence.				
ACCESSION	AL533191					
VERSION	AL533191.1	GI:12796684				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
	1 (bases 1 to 894)					
REFERENCE	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.					
AUTHORS	Full-length cDNA libraries and normalization					
TITLE	Unpublished (2001)					
JOURNAL	Contact: genoscope					
COMMENT	Genoscope - Centre National de Sequencage					
	BP 191 91006 EVRY cedex - France					
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.					
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	/clone="CS0DN003YK10"					
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	/sex="male"					
	/tissue_type="Adult brain"					
	/note="Vector: PCWVSPORT 6; Site_1: NotI; 1st strand cDNA"					

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 293 a 159 c 270 g 170 t 2 others
ORIGIN

Query Match 82.1%; Score 729.8; DB 9; Length 894;
Best Local Similarity 92.8%; Pred. No. 3.8e-151;
Matches 801; Conservative 1; Mismatches 48; Indels 13; Gaps 3;

Qy 1 GGTTTCGAGGTTTATGATCAATTCGGCTGGCAGAGAGCCCTCGCAGACAGAGCGC 60
Dy 31 GGGTTTCGGGGTTTATTGATTAATTCGGCGCGCGGGAGCCCTCGCAGAGAGAGCGC 90
Qy 61 GAGAGATGGAGATGGCAGACGGATTCAATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120
Dy 91 GAGAGATGGAGATGGCAGACGGATTCAATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 150
Qy 121 TGAAGAACTTGCCTCGACAAACAGTGGTGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Dy 151 TGAAGAACTTGTCTCGACAAACAGTGGTGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 210
Qy 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Dy 211 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCGCAA 270
Qy 241 ACTTACCAAAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
Dy 271 ACTTACCAAAAGTTAAGCAAACTTAAGAGCTTGAACCTAAGCGATACAGAGTCTCAGGGG 330
Qy 289 GCCTGGAAAGTATTGGCAAGAAAGTGTCCAAACCTCAGCGATCTATATTTAAAGTGGCAACA 348
Dy 331 GCCTGGAAAGTATTGGCAAGAAAGTGTCCGAACCTCAGCGATCTAAATTTAAAGTGGCAACA 390
Qy 349 AAATTAAGACCTCAGCACATAGAGCCACTGAACAGATTAGAAAACCTCAAGAGCTTAG 408
Dy 391 AAATTAAGACCTCAGCACATAGAGCCACTGAAAAGATTAGAAAACCTCAAGAGCTTAG 450
Qy 409 ACCTTTTCAATTGCGAGGTAAACCA-ACCTGAACGACTACGGAGAAAACGTTTCAAGCTT 467
Dy 451 ACCTTTTCAATTGCGAGGTAAACCACTTGAACGACTACCGAGAAAATGTTTCAAGCTC 510
Qy 468 CTCCTGCAACTCAGATCTCTGACAGCTGTTTACTGGACCAACAGGAGGCCCTTTACTCA 527
Dy 511 CTCCTGCAACTCAGATATCTCGAGGGCTATGACCGGACGACAGGAGGCCCTGACTCG 570
Qy 528 GATATTGAGGACCACTGGAGGGGCTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGAG 587
Dy 571 GATGCTGAGGCTACGTGGAGGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 630
Qy 588 TATGATGAAGATGCTCAGGTAGTGGAAAGTATGAGGAGGCGGAGGAGGAGGAGGAGGT 647
Dy 631 TATGATGAAGATGCTCAGGTAGTGGAAAGTATGAGGAGGCGGAGGAGGAGGAGGAGGT 690
Qy 648 GAAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGTTATACGATGAGAG 707
Dy 691 GAAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGTTATACGATGAGAG 750
Qy 708 GTAGATGGCAGGAGAGATGAAGAGAGCTTGGTGAAGAAAGAGGGGTACAGACCGAANA 767
Dy 751 GTAGATGACGAGGAGAGATGAAGAGAGCTTGGTGAAGAAAGAGGGGTACAGACCGAANA 810
Qy 768 TGAGAACTGAAGATGAGGAGAGAGATGATGACTTAAGTGAATAACCTATTTTGAANAAT 827
Dy 811 CGAAGACCTGAAGATGAGGAGAGAGATGATGACTTAAGTGAATAACCTATTTTGAANAAT 870
Qy 828 TCCTATTGTGATTGACTGTTTT 850

Db 871 TCCTATTGTGATTGACTGTTTT 893
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LOCUS AL560249 LTI_FLO11_BC1 Homo sapiens cDNA clone CS0DG002Y123 5 prime
DEFINITION , mRNA sequence.
ACCESSION AL560249 GI:12906528
VERSION AL560249
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 923)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
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/clone="CS0DG002Y123"
/clone_lib="LTI_FLO11_BC1"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 299 a 163 c 279 g 175 t 7 others
ORIGIN

Query Match 81.7%; Score 726.2; DB 9; Length 923;
Best Local Similarity 92.1%; Pred. No. 2.4e-150;
Matches 795; Conservative 6; Mismatches 49; Indels 13; Gaps 3;

Qy 1 GGTTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGAGCGC 60
Dy 62 GGGTTTCGGGGTTTATTGATTGAATTCGGCGCGGGAGCCCTCTGCAGAGAGAGAGCGC 121
Qy 61 GAGAGATGAGATGGCAGACGGATTCAATTCAGAGCTGCGGAACAGGCGCCCTCTGATG 120
Dy 122 GAGAGATGAGATGGCAGACGGATTCAATTCAGAGCTGCGGAACAGGAGCGCCCTCTGATG 181
Qy 121 TGAAGAACTTCCCTGGACACACAGTCGTCGAATCAAGGCAAACTCGAAGCCCTCACAG 180
Dy 182 TGAAGAACTTGTCTGGACACACAGTCGTCGAATGAAGGCAAACTCGAAGCCCTCACAG 241
Qy 181 ATCAATTTCAAGAACTTGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Dy 242 ATCAATTTCAAGAACTTGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCGCAA 301
Qy 241 ACTTACCAAAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
Dy 302 ACTTACCAAAAGTTAAACAAACTTAAGAACTTGAACCTTAAGCAGAGTCTCAGGGG 361
Qy 289 GCCTGGAAGTATGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348
Dy 362 GCCTGGAAGTATGGCAGAAAAGTGTCCGAACCTCAGCATCTAAATTTAAGTGGCAACA 421

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Qy 349 AAATTAAAGACCTCAGCACAAATAGAGCCACTGAACACAGTTAGAAAACCTCAAGAGCTTAG 408
|||||
Db 422 AAATTAAAGACCTCAGCACAAATAGAGCCACTGAACACAGTTAGAAAACCTCAAGAGCTTAG 481
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Qy 409 ACCTTTTCATTTGCGAGGTACCAACCTGACGACTACGGAGAAAACGTTGTTCAAGCTTC 468
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Db 482 ACCTTTTCATTTGCGAGGTACCAACCTGACGACTACCGAGAAAATGTGTTCAAGCTTC 541
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Db 542 TCCCGCAACTCACATATCTCGACGCTATGACCGGACGACAAGGAGGCCCTTACTCAG 601
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Qy 529 ATATTGAGGACCACGTCGAGGGCTTGATGACGAGGAGGAGGCTGACATGAGGAGGAGT 588
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Db 602 ATGCTGAGGGCTACGTCGAGGGCTTGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 661
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Qy 589 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 648
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Db 662 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 721
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Qy 649 AAGAGGAGGACGTCAGTGGAGGGGACGAGGAGGATGAAGAAGTTATAACGATGGAGAGG 708
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Db 722 AAGAGGAGGACGTCAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGGAGAGG 781
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Qy 709 TAGATGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGAAAAT 768
|||||
Db 782 TAGATGCGAGGAAGATGAAGAAGAGCTTGGTGAARAARAAAGGGGTCAGAAGCGAAAAC 841
|||||
Qy 769 GAGAACCTGAAGATGAGGAGAGAGATGATGACTTAAGTGAAGTAACTTATTTGAAAATTT 828
|||||
Db 842 GAGAACCTGAAGATGAGGAGAGAGATGATGACTTAAGTGAAGTAACTTATTTGAAAATTT 901
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Qy 829 CCTATTGTGATTTGACTGTTTTT 851
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Db 902 -CYATTGTGATTGACGTGTTTT 923
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RESULT 3
AL535686 875 bp mRNA linear EST 13-FEB-2001
LOCUS AL535686 LTI_FL013_FBRn1 Homo sapiens cDNA clone CS0DF016YA23 5
DEFINITION prime, mRNA sequence.
ACCESSION AL535686
VERSION AL535686.1 GI:12799179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Location/Qualifiers
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/notes="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
```

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BASE COUNT 291 a 156 c 287 g 160 t 1 others
ORIGIN
Query Match 81.5%; Score 724.2; DB 9; Length 875;
Best Local Similarity 92.9%; Pred. No. 6.e-150;
Matches 785; Conservative 0; Mismatches 48; Indels 12; Gaps 2;
Qy 1 GGGTTCAGAGTTTATTGATTGGAATTCGGCTGGCAGCAGAGAGCCCTCTGCAGACAGAGAGCGC 60
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Db 31 GGGTTCGGGTTTATTGATTGGAATTCGGCGGGGAGCCCTCTGCAGAGAGAGAGCGC 90
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Qy 61 GAGAGATGAGAGATGGCCACACGAGATTCAATTCAGAGCTCGGGAACAGGGCCCTCTGTGATG 120
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Db 91 GAGAGATGAGAGATGGCCACACGAGATTCAATTCAGAGCTCGGGAACAGGGCCCTCTGTGATG 150
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Qy 181 ATGAATTTGAAGAAGCTGGGAATTTCTTAAGTAAATCAACGAGGAGCCCTCACCTCAATCTCAG 240
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Qy 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTTGAACCTA-----AGAGTCTCAGGGG 288
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Qy 289 GCGTGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAACTGCGCAACA 348
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Db 331 GCGTGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCATCTAAATTTAAGTGGCAACA 390
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Qy 349 AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
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Qy 409 ACCTTTTCAATTGCGAGGTAAACCAACCTGACGACTACGGAGAAAACGTTGTTCAAGCTTC 468
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Db 451 ACCTTTTCAATTGCGAGGTAAACCAACCTGACGACTACGGAGAAAATGTGTTCAAGCTTC 510
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Qy 469 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAGGAGGCCCTTACTCAG 528
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Db 511 TCCCGCAACTCACATATCTCGACGCTATGACCGGACGACAGGAGGCCCTTACTCAG 570
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Qy 589 ATGATGAAGATGCTCAGGTAGTGGAGAGATGAGGAGGGCCGAGGAGGAGGAGGAGGAGT 648
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Db 691 AAGAGGAGGACGTCAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGGAGAGG 750
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Qy 709 TAGATGGCAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGAAAAT 768
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Qy 769 GAGAACCTGAAGATGAGGAGAGAGATGATGACTTAAGTGAAGTAACTTATTTGAAAATTT 828
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Qy 829 CCTAT 833
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Db 871 CCTAT 875
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RESULT 4
AL518839
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ORIGIN

Query Match	79.8%	Score 709.4	DB 9	Length 870
Best Local Similarity	92.2%	Pred. No. 1.2e-146		
Matches 772	Conservative 1	Mismatches 52	Indels 12	Gaps 2
QY	1	GGGTTTCGAGGTTTATTGATTCGAATTCGGCTGGCACGAGAGCCCTGTCGACAGACGAGAGCCG	60	
Db				
Db	31	GGGTTTCGCGGTTTATTGATTGAATTCGCGCGCGCGGAGCCCTCTCGAGAGAGAGAGCCG	90	
QY	61	GAGAGATGGAGATGGGCAGACGGGATTCATTCAGAGCTGCGGAAACAGGGCGCCCTCTGATG	120	
Db				
Db	91	GAGAGATGGAGATGGGCAGACGGGATTCATTCAGAGCTGCGGAAACAGGGCGCCCTCTGATG	150	
QY	121	TGAAAGAACTTGCCCTGGACACACAGTCGGTCGAATGAAGCAACACGTCGAGGCCCTCACAG	180	
Db				
Db	151	TGAAGAACTTGCTCGGACACACAGTCGGTCGAATGAAGCAACACGTCGAGGCCCTCACAG	210	
QY	181	ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG	240	
Db				
Db	211	ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGTAGGCCCTCACCTCAATCGCAA	270	
QY	241	ACTTACCAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGGG	288	
Db				
Db	271	ACTTACCAAGTTAACAACAACTTAAAGAGCTTGAACCTAAGCGATACAGAGTCTCAGGGG	330	
QY	289	GCCTGGAAAGTATGGCAGAAAGTGTCGCAACCTCAGGCATCTATATTTAAGTGGGCAACA	348	
Db				
Db	331	GCCTGGAAGTATGGCAGAAAGTGTCGCAACCTCAGGCATCTAATTTAAGTGGGCAACA	390	
QY	349	AAATTTAAGACCTCAGCAACAATAGAGCCACTGAACAGTTAGAAAAACCTCAAGAGCTTAG	408	
Db				
Db	391	AAATTTAAGACCTCAGCAACAATAGAGCCACTGAAAAAGTTAGAAAAACCTCAAGAGCTTAG	450	
QY	409	ACCTTTTCAATTCGCGAGTACCAACCTGACGACCTACGGAGAAAACGTTCTCAAGCTTC	468	
Db				
Db	451	ACCTTTTCAATTCGCGAGTACCAACCTGACGACCTACCGAGAAAATGTTCTCAAGCTCC	510	
QY	469	TCCTGCAACTCACATATCTGCACAGCTGTTTACTTGGGACCACAGAGAGGCCCTTACTCAG	528	
Db				
Db	511	TCCTGCAACTCACATATCTGCACAGCTGTTTACTTGGGACCACAGAGAGGCCCTTACTCAG	570	
QY	529	ATATTGAGACCACTGGAGGCCCTGATGACGAGGAGGAGGTGATGATGAGGAGGAGT	588	
Db				
Db	571	ATGCTGAGGGCTACGTTGGAGGCCCTGGATGATGAGGAGGAGTATGAGTATGAGGAGGAGT	630	
QY	589	ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCCGAGGAGGAGGAGGAGGAGT	648	
Db				
Db	631	ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCCGAGGAGGAGGAGGAGGAGT	690	
QY	649	AAAGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAAGCTTTATACGATGGAGAG	708	
Db				
Db	691	AAAGAGGAGCTGAGTGGAGGAGGAGGAGGATGAAGAAGCTTTATACGATGGAGAGG	750	
QY	709	TAGATTGGCGAGGAGAGATCAAGAAAGCTTGCTGAAGAAGAAAGGGTTCAGAGCCGAAAT	768	
Db				
Db	751	TASATGACGAGGAGATGAAGAGAGCTTGCTGAGAGAGAAACGGGTCAAGACCGAAAC	810	
QY	769	GAGAACCTGAAGATGAGGAGGAGAGATGATGACTAAGTAGAATTAACCTATTTTGA	825	
Db				
Db	811	GAGAACCTGAAGATGAGGAGGAGAGATGATGACTAAGTGAATTAACCTATTTTGA	867	

RESULT 6	AL547157	AL547157	875 bp	mRNA	linear	EST 27-FEB-2001
LOCUS	AL547157	AL547157	875 bp	mRNA	linear	EST 27-FEB-2001
DEFINITION	AL547157	AL547157	875 bp	mRNA	linear	EST 27-FEB-2001
ACCESSION	AL547157	AL547157	875 bp	mRNA	linear	EST 27-FEB-2001
VERSION	AL547157.1	AL547157.1	875 bp	mRNA	linear	EST 27-FEB-2001
KEYWORDS	AL547157.1	AL547157.1	875 bp	mRNA	linear	EST 27-FEB-2001
SOURCE	AL547157.1	AL547157.1	875 bp	mRNA	linear	EST 27-FEB-2001
ORGANISM	AL547157.1	AL547157.1	875 bp	mRNA	linear	EST 27-FEB-2001

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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FEATURES	SOURCE
1. <u>Age</u>	1. <u>Age</u>
2. <u>Gender</u>	2. <u>Gender</u>
3. <u>Marital Status</u>	3. <u>Marital Status</u>
4. <u>Education</u>	4. <u>Education</u>
5. <u>Income</u>	5. <u>Income</u>
6. <u>Occupation</u>	6. <u>Occupation</u>
7. <u>Religion</u>	7. <u>Religion</u>
8. <u>Political Affiliation</u>	8. <u>Political Affiliation</u>
9. <u>Health Status</u>	9. <u>Health Status</u>
10. <u>Travel History</u>	10. <u>Travel History</u>
11. <u>Employment Status</u>	11. <u>Employment Status</u>
12. <u>Family Size</u>	12. <u>Family Size</u>
13. <u>Home Ownership</u>	13. <u>Home Ownership</u>
14. <u>Vehicle Ownership</u>	14. <u>Vehicle Ownership</u>
15. <u>Insurance Status</u>	15. <u>Insurance Status</u>
16. <u>Subscription Services</u>	16. <u>Subscription Services</u>
17. <u>Charitable Donations</u>	17. <u>Charitable Donations</u>
18. <u>Volunteer Work</u>	18. <u>Volunteer Work</u>
19. <u>Political Participation</u>	19. <u>Political Participation</u>
20. <u>Healthcare Usage</u>	20. <u>Healthcare Usage</u>
21. <u>Travel Frequency</u>	21. <u>Travel Frequency</u>
22. <u>Employment Duration</u>	22. <u>Employment Duration</u>
23. <u>Family Income</u>	23. <u>Family Income</u>
24. <u>Home Value</u>	24. <u>Home Value</u>
25. <u>Vehicle Type</u>	25. <u>Vehicle Type</u>
26. <u>Insurance Type</u>	26. <u>Insurance Type</u>
27. <u>Subscription Type</u>	27. <u>Subscription Type</u>
28. <u>Charitable Type</u>	28. <u>Charitable Type</u>
29. <u>Volunteer Type</u>	29. <u>Volunteer Type</u>
30. <u>Political Type</u>	30. <u>Political Type</u>
31. <u>Healthcare Type</u>	31. <u>Healthcare Type</u>
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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was primed with a NotI-oligo(dT) primer.. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : flliang@lifetech.com URL :
http://flliang@lifetech.com"

```

```

BASE COUNT
ORIGIN
288 a 157 c 267 g 161 t 2 others
http://ruiheng.cn.invtrojan.com

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Best Local Similarity 92.4%; Pred. No. 7.7e-146;
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QY	61	GAGAGATGGAGATGGGCAGACGAGATTCATTTCAGAGCTGCGGAACAGAGGCGCCCTCTGATG	120
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QY	241	ACTTACCAAAAGTTA--AACTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGG	288
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QY	289	GCCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTTCAGGCATCTATATTAAAGTGGCAACA	348
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VERSION AL540827.1 GI:12871345
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 298 a 160 c 271 g 164 t 10 others
ORIGIN

Query Match 79.3%; Score 705.4; DB 9; Length 903;
Best Local Similarity 91.7%; Pred. No. 9,5e-146;
Matches 773; Conservative 8; Mismatches 49; Indels 13; Gaps 3;

QY 1 GGGTTGAGGTTTATGATGAATTCGGCTGGCAGCAGAGAGGCTCTGCAGACAGAGAGCGC 60
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Db 112 GAAAAAGGAGAGAGGAGGAGAGGATTCATTTAGAGCTGCGGAACAGAGGACGCTCTGATG 171
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Db 172 TGAARAAGACTTGCTCTGGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCTCACAG 231
QY 181 ATGAATTTGAAGAACTGGATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
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Db 232 ATGAATTTGAAGAACTGGATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCGCAA 291
QY 241 ACTTACCAAGTTA---AGTTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
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DEFINITION AL517375 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA003YC02 5
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ACCESSION AL517375
VERSION AL517375.1 GI:12780868
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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ORIGIN	11 others	
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SOURCE human.		
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AUTHORS NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT Unpublished (1999)		
Contact: Robert Strausberg, Ph.D.		
Email: cgepbs-r@mail.nih.gov		
Tissue Procurement: Lou Staudt		
cDNA Library Preparation: Life Technologies, Inc.		
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
DNA Sequencing by: Agencourt Bioscience Corporation		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:		
http://image.llnl.gov		
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Best Local Similarity 88.6%; Pred. No. 6.8e-142;		
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Qy	121	TGAAGAACTTGCCTTGGACAAAGTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
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Db 767 TAGATGGCGAGCAAGTGAAGAGAGCTGGTGAAGAGAAAGGGGTGAGAGGCAAAAC 826
QY 769 GAGAACTGAAGATGAGGAGGAGGAGTGTGACTAAGTGAAGATAAC--TATTTTGAAGAA 826
Db 827 GAGCACTGAGATGAGGAGGAGGAGGAGTGTGACTAAGTGAAGATAACCTTATTTTGAAGAA 886
QY 827 TTCCCTATTGATTGACTG---TTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCC 881
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RESULT 10
AL543743 855 bp mRNA linear EST 16-FEB-2001
LOCUS AL543743 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI005YK13 5
DEFINITION prime, mRNA sequence.
ACCESSION AL543743
VERSION AL543743.1 GI:12876222
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 855)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..855
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/clone_lib="LTI_NFL006_PL2"

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/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

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BASE COUNT 280 a 151 c 265 g 152 t 7 others
ORIGIN

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Query Match 76.9%; Score 683.8; DB 9; Length 855;
Best Local Similarity 92.0%; Pred. No. 5.6e-141;
Matches 752; Conservative 5; Mismatches 47; Indels 13; Gaps 3;

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QY 1 GGGTTCGAGGTTTATTGATTTCGGCTGGCCAGAGAGCCCTCTGCAGACAGAGAGCGC 60
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QY 61 GAGAGATGGAGATGGCGAGACGAGTTCATTGAGCTGCGGAACAGGGCCCTCTGATG 120
Db 100 GAGAGATGGAGATGGCGAGACGAGTTCATTGAGCTGCGGAACAGGGCCCTCTGATG 159
QY 121 TGAAGAAGACTTGGCCCTGGCAACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 160 TGAAGAAGACTTGGCCCTGGCAACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCCTCACAG 219
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAAATCAACGAGGAGCCCTCACCTCAATCTCAG 240
Db 220 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAAATCAACGAGGAGCCCTCACCTCAATCTCAG 279
QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAAGTA-----AGAGTCTCAGGGG 288
Db 280 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAAGTA-----AGAGTCTCAGGGG 339
QY 289 GCGTGGAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348
Db 340 GCGTGGAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 399
QY 349 AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 400 AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 459
QY 409 ACCTTTTCAATTCGAGGTAAACCACTGACGAGTAAACGAGTAAACGAGTAAACGAGTAA 468
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QY 469 TCCTGCAACTCATATCTCGACAGCTGTTACTGGGACCAAGGAGGCCCTTACTCAG 528
Db 520 TCCCGCAACTCATATCTCGACAGCTATGACCGGGACGACAAGGAGGCCCTGACTCGG 579
QY 529 ATATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 588
Db 580 ATGCTGAGGGCTACGTGGAGGGCTTGGATGATGAGGAGGAGGAGGAGGAGGAGGAGT 639
QY 589 ATGATGAAGTCTCAGGTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 648
Db 640 ATGATGAAGTCTCAGGTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 699
QY 649 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
Db 700 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 759
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Db 760 TAGATGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 819
QY 769 GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 805
Db 820 GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 855

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RESULT 11
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LOCUS AL535863 LTI_FL013_FBrnl 853 bp mRNA linear EST 13-FEB-2001
DEFINITION AL535863 LTI_FL013_FBrnl Homo sapiens cDNA clone CS0DF013J23 5
prime, mRNA sequence.
ACCESSION AL535863
VERSION AL535863
KEYWORDS EST.
SOURCE AL535863.1 GI:12799356
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 853)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/clone_lib="LTI_FL013_FBrnl"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and enriched into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 283 a 147 c 254 g 164 t 5 others
ORIGIN
Query Match 75.2%; Score 668.6; DB 9; Length 853;
Best Local Similarity 90.3%; Pred. No. 1.3e-137;
Matches 770; Conservative 5; Mismatches 59; Indels 19; Gaps 5;
QY 17 GATTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAGAGCGCGAGATGGAGATGGG 76
Db 1 GATTGAATTCGGCGCGGGAGCCCTCTGCAGAGAGAGCGCGAGATGGAGATGGG 60
QY 77 CAGACGGATTCAATTCAGAGCTGCGGAACAGGGCGCCCTCTGATGTGAAAGAACTTGCCT 136
Db 61 CAGACGGATTCAATTCAGAGCTGCGGAACAGAGCGCCCTCTGATGTGAAAGAACTTGCCT 120
QY 137 GGACACAGTCGGTCGATGAAGCAACTCGAACCCCTCACATGAATTTGAAGAACT 196
Db 121 GGACACAGTCGGTCGATGAAGCAACTCGAACCCCTCACATGAATTTGAAGAACT 180
QY 197 GGAATCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAGACTTACCAAGTTA-- 254
Db 181 GGAATCTTAAGTAAATCAACGTAGGCGCTCACCTCAATCTCAGACTTACCAAGTTAA 240
QY 255 -AAGTTGAGAAGCTTGAACTA-----AGAGTCTCAGGGGGCGCTGGAAGTATTGGC 304
Db 241 CAAACTTAAGAAGCTTGAACCTAAGCGATAACAGAGTCTCAGGGGCGCTGGAAGTATTGGC 300
QY 305 AGAAAAGTGTCCAAACCTCAGCATCTATATTAAAGTGGCAACAAAATTAAGACCTCAG 364
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QY 365 CACAATAGCACCTGAACAGTGTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTGGCA 424
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361 CACAATAGCACCTGAACAGTGTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTGGCGA 420
QY 425 GGTAAACCACTGAACGACTACGAGAGAAAACGTTGTCAAGCTTCTCTCGCAACTCACATA 484
Db 421 GGTAAACCACTGAACGACTACGAGAGAAAATGTGTTCACAGCTCTCTCCGCAACTCACATA 480
QY 485 TCTCGACAGCTGTACTGGGACCAACAGAGGAGGCCCTTACTCAGATATATTGAGG---ACC 540
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QY 541 ACCTGAGGGCCCTGGATGACGAG-GAGGAGGGTGAG--CATGAGGAGGAGTATGATGAAG 597
Db 541 GTGGTAGGTCCTGGATGATGACTGAGGAGGATGAGGTATGAGTATGAGTATGATGAAG 600
QY 598 ATGCTCAGGTAGTGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 657
Db 601 ATGCTCAGGTAGTGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 658 ACCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 717
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QY 718 AGGAAGATGAAGAGAGCTTGGTGAAGAAAGAGGGTTCAGAAAGCGAAAGTATGAAACCTG 777
Db 721 AGCAAGATGAAGAGAGCTTGGTGAAGAAAGAGGGTTCAGAAAGCGAAAGTATGAAACCTG 780
QY 778 AAGATGAGGAGAGATGATGACTAAGTAGAATAAAGTATTTGAAAAATTCCTATTGTG 837
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QY 838 ATTGTGACTGTTTT 850
Db 841 ATTGTGACTGTTTT 853
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DEFINITION AL545880 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI023YE09 5
prime, mRNA sequence.
ACCESSION AL545880
VERSION AL545880
KEYWORDS EST.
SOURCE AL545880.1 GI:12878473
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 834)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
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BASE COUNT.	272 a	153 c	257 g	148 t	4 others
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Query Match	74.9%; Score 665.6; DB 9; Length 834;				
Best Local Similarity	92.1%; Pred. No. 5.9e-137;				
Matches 724; Conservative	3; Mismatches 47; Indels 12; Gaps 2;				
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QY	61	GAGAGATGAGATGGCAGACGGATTTCATTCAGAGCTCGGGAACAGGGCCCTCTGATG	120		
Db	105	GARARATGAGATGGCAGACGGATTTCATTTAGAGCTCGGGAACAGGACGGCCCTCTGATG	164		
QY	121	TGAAGAACTTCGCCCTGGACACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCCTCCACAG	180		
Db	165	TGAAGAACTTCGCCCTGGACACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCCTCCACAG	224		
QY	181	ATGAATTTGAAGAACTGGAATTTTAAAGTAAATCAACGGAGCGCTCACCTCAATCTCAG	240		
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QY	241	ACTTACCAAGTTA---AGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG	288		
Db	285	ACTTACCAAGTTAACAACAACTTAAGAAGCTTGAACCTAAGCGATTAACAGAGCTCTCAGGGG	344		
QY	289	GCCTGGAAGTATTGGCAGAAAAGTCTCAAACTCCACGCATCTATATTTAAAGTGGCAACA	348		
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QY	349	AAATTAAGACCTCAGCACAANTAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG	408		
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QY	469	TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCAACAGGAGGCCCTTACTCTAG	528		
Db	525	TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCAACAGGAGGCCCTTACTCTAG	584		
QY	529	ATATTGAGGACACCTGGAGGCGCTTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGAGT	588		
Db	585	ATGCTGAGGCTACCTGGAGGCGCTTGGATGACGAGGAGGAGGATGAGCATGAGGAGGAGT	644		
QY	589	ATGATGAAGATCCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGTG	648		
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QY	649	AAGAGGAGGACCTGAGTGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGAGAGG	708		
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QY	709	TAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAGGCGAAAT	768		
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QY	769	GAGAAC	774		
Db	825	GAGAAC	830		
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ACCESSION	BQ232856				
VERSION	BQ232856.1 GI:20414256				
KEYWORDS	5', mRNA sequence.				
SOURCE	human.				

ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 895)				
TITLE	NIH-MGC http://mgi.nci.nih.gov/.				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
CONTACT	Contact: Robert Strausberg, Ph.D.				
EMAIL	Email: cgabs-r@mail.nih.gov				
TISSUE	Tissue Procurement: DCTD/Drp/Gazdar				
CDNA	CDNA Library Preparation: Life Technologies, Inc.				
DNA	DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)				
CLONE	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:				
PLATE	http://image.llnl.gov				
PLATE	Plate: LLAM13328 row: n column: 12				
FEATURES	High quality sequence stop: 676.				
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	/clone_lib="NIH_MGC_68"				
	/tissue_type="large cell carcinoma"				
	/lab_host="DH10B (phage-resistant)"				
	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."				
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Query Match	74.4%; Score 661; DB 14; Length 895;				
Best Local Similarity	92.0%; Pred. No. 6.2e-136;				
Matches 736; Conservative	0; Mismatches 51; Indels 15; Gaps 5;				
QY	1	GGGTCGAGGTTTATGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGAGCGC	60		
Db	46	GGGTCGCGGTTTATGATTGAATTCGGCGCGCGGGAGCCCTCTGCAGAGAGAGAGCGC	105		
QY	61	GAGAGATGAGATGGGAGACGGATTTCATTTCAGAGCTGGGAACAGGGCCCTCTGTATG	120		
Db	106	GAGAGATGAGATGGGAGACGGATTTCATTTCAGAGCTGGGAACAGGGCCCTCTGTATG	165		
QY	121	TGAAGAACTTCGCCCTGGACACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCCTCCACAG	180		
Db	166	TGAAGAACTTCGCCCTGGACACAGCTCGGTGCAATGAAGGCAAACTCGAAGCCCTCCACAG	225		
QY	181	ATGAATTTGAAGAACTGGAATTTTAAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG	240		
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QY	241	ACTTACCAAGTTA---AGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG	288		
Db	286	ACTTACCAAGTTTAAACAACTTAAAGAAAGCTTGAACCTAAGCGATAACAGAGTCTCAGGGG	345		
QY	289	GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGGCATCTATATTTAAAGTGGCAACA	348		
Db	346	GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGGCATCTATAATTTAAAGTGGCAACA	405		
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QY	409	ACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAGAAACGTGTTCAAGCTTC	468		
Db	466	ACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAGAAACGTGTTTCAAGCTTC	525		
QY	469	TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCAACAGGAGGCCCTTACTCTAG	528		
Db	526	TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCAACAGGAGGCCCTTACTCTAG	585		

Db	61	GTGAAGAACCTTGTCTGGACAACAGTCGGTGAATGAAGCAAACTCGAAGGCGCTCAC		120	
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QY	240	GACTTTACCAAAAGTTTAA--AGTTTGAGAAAGCTTTGAACCTA-----AGAGTCTCAGGG	287		
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QY	288	GGCCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTTACGCATCTATATATTTAAGTGGCAAC	347		
Db	241	GGCCTGGAAGTATTGGCAGAAAAAGTGTCCGAACCTTCAACATCTAAATTTAAGTGGCAAC	300		
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QY	408	GACCTTTTCAATTCGGAGGTAAACCAACCTTGAACGACTACCGAGAGAAACCTGTTTCAAGCTTT	467		
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QY	468	CTCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAGAGAGGCCCTTACTCA	527		
Db	421	CTCCGCAACTCACATATCTCGACGGCTATGACCGGAGCAGCAAGGAGGCCCTTGACTCG	480		
QY	528	GATATTGAGGACCACTGGAGGGCTTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGAG	587		
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QY	588	TATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGT	647		
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QY	648	GAGAGGAGGAGCTCAGTGGAGGGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGGAGAG	707		
Db	601	GAGAGGAGGAGCTCAGTGGAGGGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGGAGAG	666		
QY	708	GTAGATGGCGAGGAGAGATGAAGAAGAGCTTTGGTGAAGAAGAAGGGGTCAGAGCGAANA	767		
Db	661	GTAGATGACGAGGAAGATGAAGAAGAAGCTTTGGTGAAGAAGA--GGGTGAGAAGCGAANA	719		
QY	768	TGAGAACCTTGAG--ATGAGGAGAGAGATGATGACTAAGTAGAATAA--CCTATTTTGAANA	822		
Db	720	CGAGAACCTTGAAGATGAGGAGAGAGATGATGACTAAGTAGAATAA--CCTATTTTGAANA	779		
QY	826	ATTCTTATTGTTGATTGACTGTTTATTACCCAT-----ATCCCCCTCCCCCTCCCAATC	877		
Db	780	AATCCAATTGGGATTGACTGGTTTTTACCCTTATTTCCCTTTTCCCTCCCCCTCCCAATC	833		
QY	878	CTGCCCCCTGAA 889			
Db	840	CTGCCCCCTGAA 851			
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LOCUS	AL571434	LTI_NFL006_PL2	894 bp	mRNA	linear
DEFINITION	AL571434	prime, mRNA	894 bp	894 bp	EST 16-PEP
ACCESSION	AL571434	GI:12928726			EST
VERSION	AL571434.1				human
KEYWORDS	EST				human
SOURCE	human				human
ORGANISM	human				human
REFERENCE	AL571434	human			human
AUTHORS	Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.				human
TITLE	Full-length cDNA libraries and normalization				human
JOURNAL	Unpublished (2001)				human
COMMENT	Contact: Genoscope				human

